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OM protein - protein search, using sw model

Run on: January 10, 2005, 21:05:23 ; Search time 153 Seconds  
(without alignments)  
940.199 Million cell updates/sec

Title: US-09-813-718-10\_COPY\_71\_471

Perfect score: 2116

Sequence: 1 SNHGPDATEABEDFVDPWTV.....VTDEIVKFWTPRKLSFDQ 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2116	100.0	401	5	AAG79549 TrpRS T1
2	2116	100.0	415	4	AAB47617 Human sup
3	2116	100.0	415	5	AAE13493 Human sup
4	2116	100.0	415	5	AAG79548 His6-tag
5	2116	100.0	415	6	ABU72386 Human sup
6	2116	100.0	437	4	AAB47616 Human min
7	2116	100.0	437	5	AAE13492 Human min
8	2116	100.0	437	5	AAG79547 His6-tag
9	2116	100.0	437	6	ABU72385 Human min
10	2116	100.0	471	7	ADF76576 Novel hum
11	2116	100.0	471	7	ABU64298 Human try
12	2116	100.0	471	7	ADN39916 Cancer/an
13	2116	100.0	471	8	ADJ75318 Marker ge
14	2116	100.0	471	8	ADP12573 Protein e
15	2116	100.0	484	4	AAB47615 Human ful
16	2116	100.0	484	5	AAE13491 Human try
17	2116	100.0	484	5	AAG79546 Full leng
18	2116	100.0	484	6	ABU72384 Human ful
19	2101	99.3	471	7	ADE25762 Human pro
20	2101	99.3	471	7	ADJ69429 Human hea
21	2101	99.3	471	8	ADE76998 Human pro
22	2101	99.3	471	8	ADQ30575 Pancreas
23	2101	99.3	475	3	AAB58220 Lung canc
24	2096	99.1	471	2	AAY05372 Human HCM
25	1988	94.0	378	5	AAG79541 TrpRS T2

26	1988	94.0	392	4	AAB47618	Aab47618 Human ina
27	1988	94.0	392	5	AAE13494	Aae13494 Human ina
28	1988	94.0	392	5	AAG79544	Aag79544 His6-tag
29	1988	94.0	392	6	ABU72387	Abu72387 Human min
30	1988	94.0	392	8	ADJ87004	Adj87004 His-tagge
31	1973	93.2	378	6	AAG79953	Aag79953 T2-TrpRS
32	1938	91.6	475	7	ADB79825	Adb79825 Mouse put
33	1938	91.6	481	8	ADJ76140	Adj76140 Marker ge
34	1459.5	69.0	447	8	ADP04555	Adp04555 Sea squir
35	1370.5	64.8	430	4	ABB64621	Abb64621 Drosophil
36	1370.5	64.8	430	4	ABB67203	Abb67203 Drosophil
37	1304	61.6	402	3	AAG23698	Aag23698 Arabidops
38	1304	61.6	426	3	AAG23697	Aag23697 Arabidops
39	1218.5	57.6	424	4	AAB66931	Aab66931 Tryptopha
40	1200.5	56.7	424	5	ABP73795	Abp73795 Candida a
41	1163	55.0	432	6	ABR53898	AbR53898 Protein e
42	1163	55.0	432	7	ADK64828	Adk64828 Disease t
43	1125	53.2	433	6	ABJ26487	Abj26487 Aspergill
44	1107.5	52.3	456	7	ADB70160	Adb70160 C. neofor
45	968	45.7	292	3	AAG23699	Aag23699 Arabidops

#### ALIGNMENTS

RESULT 1

AAG79549

ID AAG79549 standard; protein; 401 AA.

XX AAG79549;

XX

DT 10-DEC-2002 (first entry)

XX

DE TrpRS T1 polypeptide.

XX

KW T2; tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation;

KW neovascular eye disease; age-related macular degeneration;

KW ocular complication; diabetes; rubecotic glaucoma; retinopathy;

KW prematurity; keratitis; ischaemic retinopathy; sickle cell;

KW pathological myopic; ocular histoplasmosis; pterygia; T1;

KW puniate innerchoroidopathy; retinal degeneration; growth factor;

KW vascularisation; vascular endothelial cell function; angiogenesis.

XX

OS Homo sapiens.

XX

PN WO200267970-A1.

XX

PD 06-SEP-2002.

XX

XX 22-FEB-2002; 2002WO-US005185.

XX

PR 23-FEB-2001; 2001US-0270951P.

XX

PA (SCRI ) SCRIPPS RES INST.

XX

XX Schimmel P, Wakasugi K, Friedlander M;

XX

XX WPI; 2002-698635/75.

XX

PT New polypeptides derived from human tryptophanyl-tRNA synthase, useful for inhibiting ocular neovascularization in a patient, or for treating neovascular eye diseases, e.g. rubecotic glaucoma, retinopathy, keratitis, or pterygia.

XX

PS Example 1; Page 78-79; 83pp; English.

XX

CC This sequence represents a novel cleavage product, T1, of recombinant human tryptophanyl-tRNA synthase (TrpRS). A related cleavage product, T2, is water soluble and comprises residues 94-471 of full length TrpRS. The water-soluble T2 polypeptide is useful for inhibiting ocular neovascularisation in a patient. The T2 polypeptide is useful for treating neovascular eye diseases, e.g. age-related macular degeneration, ocular complications of diabetes, rubecotic glaucoma, retinopathy of

CC prematurity, keratitis, ischaemic retinopathy (e.g. sickle cell),  
CC pathological myopic, ocular histoplasmosis, pterygia, or punctate  
CC innerchorioidopathy. This polypeptide is particularly useful for treating  
CC retinal degeneration to prevent the damaging effects of trophic and  
CC growth factors, and for promoting vascularisation to retard retinal  
CC degeneration by enhancing blood flow to cells. These are also useful for  
CC regulating vascular endothelial cell function, and in particular, for  
CC inhibiting angiogenesis  
XX  
SQ Sequence 401 AA;

Query Match 100.0%; Score 2116; DB 5; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.6e-209;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SNHGPDTEAEEDFVDPWVTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 60  
DB 1 SNHGPDTEAEEDFVDPWVTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 60  
QY 61 FLRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMHVGHLPFTKWLQDVFNVP 120  
DB 61 FLRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMHVGHLPFTKWLQDVFNVP 120  
QY 121 LVIQMTDDEKYLKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFYKN 180  
DB 121 LVIQMTDDEKYLKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFYKN 180  
QY 181 VVKIQKHVTFNQVKGIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCA 240  
DB 181 VVKIQKHVTFNQVKGIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCA 240  
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSIFLDTAKQIKT 300  
DB 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSIFLDTAKQIKT 300  
QY 301 KVNKHFSGGRDTEEHROFGNCNDVVSFWYLTFFLEDDDDKLEQIRKDYTSGLMTGEL 360  
DB 301 KVNKHFSGGRDTEEHROFGNCNDVVSFWYLTFFLEDDDDKLEQIRKDYTSGLMTGEL 360  
QY 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMTPRKLSFDFQ 401  
DB 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMTPRKLSFDFQ 401

RESULT 2  
ID AAB47617 standard; protein; 415 AA.  
XX AAB47617;  
AC AAB47617;  
DT 07-JAN-2002 (first entry)  
XX Human supermini TrpRS.  
DE Tyrosyl-tRNA synthetase; TrpRS; Rossmann fold nucleotide binding domain;  
KW vascular endothelial cell function; burn; plastic surgery; abdomen;  
KW polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis;  
KW angiogenesis; graft; myocardial infarction; solid tumour; wound healing;  
KW dermal ulcer; diabetic ulcer; endothelialization;  
KW tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.  
XX  
OS Homo sapiens.  
XX WO200174841-A1.  
PN 11-OCT-2001.  
PD 21-MAR-2001; 2001WO-US008966.  
PF 31-MAR-2000; 2000US-0193471P.  
PR (SCRI ) SCRIPPS RES INST.  
XX  
PA XX

PI Schimmel P, Wakasugi K;  
XX WPI; 2001-626377/72.  
DR N-PSDB; AAH43604.  
XX New human truncated tyrosyl-tRNA synthetase polypeptide for regulating  
PT vascular endothelial function, in particular for regulating angiogenesis,  
PT tumor metastasis and treating myocardial infarction.  
XX  
PS Disclosure; Page 129-30; 150pp; English.  
XX

XX The sequences given in AAB47615-18 show full length and truncated  
CC versions of tryptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of  
CC the invention comprises a Rossmann fold nucleotide binding domain, and is  
CC capable of regulating vascular endothelial cell function. It is of  
CC approx. 40 kilo Dalton molecular weight and is produced by cleavage of  
CC full length TrpRS with polymorphonuclear leucocyte elastase. Truncated  
CC TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing  
CC angiogenesis to a graft, treating myocardial infarction, solid tumor, and  
CC a condition that would benefit from increased or decreased angiogenesis  
CC in a mammal, in particular humans. It is also useful in diagnosis and as  
CC a wound healing agent for treating wounds such as dermal ulcers, diabetic  
CC ulcers, burns and injuries and in plastic surgery when reconstruction is  
CC required following a burn or for cosmetic purposes. It is particularly  
CC useful in the treatment of abdominal wounds where there is high risk of  
CC infection. Truncated TrpRS promotes endothelialization in vascular graft  
CC surgery and is used in conjunction with angiography to administer the  
CC angiogenic trpRS synthetase polypeptides or polynucleotides directly to  
CC the lumen and wall of the blood vessel  
XX  
SQ Sequence 415 AA;

Query Match 100.0%; Score 2116; DB 4; Length 415;  
Best Local Similarity 100.0%; Pred. No. 1.7e-209;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SNHGPDTEAEEDFVDPWVTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 60  
DB 2 SNHGPDTEAEEDFVDPWVTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 61  
QY 61 FLRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMHVGHLPFTKWLQDVFNVP 120  
DB 62 FLRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMHVGHLPFTKWLQDVFNVP 121  
QY 121 LVIQMTDDEKYLKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFYKN 180  
DB 122 LVIQMTDDEKYLKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFYKN 181  
QY 181 VVKIQKHVTFNQVKGIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCA 240  
DB 182 VVKIQKHVTFNQVKGIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCA 241  
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSIFLDTAKQIKT 300  
DB 242 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSIFLDTAKQIKT 301  
QY 301 KVNKHFSGGRDTEEHROFGNCNDVVSFWYLTFFLEDDDDKLEQIRKDYTSGLMTGEL 360  
DB 302 KVNKHFSGGRDTEEHROFGNCNDVVSFWYLTFFLEDDDDKLEQIRKDYTSGLMTGEL 361  
QY 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMTPRKLSFDFQ 401  
DB 362 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMTPRKLSFDFQ 402

RESULT 3  
ID AAE13493 standard; protein; 415 AA.  
XX AAE13493;  
AC AAE13493;  
XX 12-FEB-2002 (first entry)  
DT XX  
XX

Db	62	FLRRGIFFSHRDNNQVLDAVENKPFYLYTGRGSPSSAMHVGHLIPFTFTKWLQDVFNVP	121
Qy	121	LVLTQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFFISDLIDYMGSSGFYKN	180
Db	122	LVLTQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFFISDLIDYMGSSGFYKN	181
Qy	181	VVKIQKHVTNQVKGIFGFTSDCIGIKISPPAIOAAPSFSNSPFOIFRDRTDIOCLIFCA	240
Db	182	VVKIQKHVTNQVKGIFGFTSDCIGIKISPPAIOAAPSFSNSPFOIFRDRTDIOCLIFCA	241
Qy	241	IDQDPYFRMTRDVAPRIGYPKPAALLHSTFPPALOGAOTKMSASDPNSSIFLTDTAQIKT	300
Db	242	IDQDPYFRMTRDVAPRIGYPKPAALLHSTFPPALOGAOTKMSASDPNSSIFLTDTAQIKT	301
Qy	301	KVKAGHAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL	360
Db	302	KVKAGHAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL	361
Qy	361	KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSPDFQ	401
Db	362	KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSPDFQ	402
RESULT 4			
AAG79548			
ID AAG79548 standard; protein; 415 AA.			
XX	AC	AAG79548;	
XX	AC		
XX	XX		
DT	10-DEC-2002	(first entry)	
XX	XX		
XX	XX	His6-tagged TrpRS T1 polypeptide.	
KW	KW	T2; tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation;	
KW	KW	neovascular eye disease; age-related macular degeneration;	
KW	KW	ocular complication; diabetes; rubecotic glaucoma; retinopathy;	
KW	KW	prematurity; keratitis; ischaemic retinopathy; sickle cell;	
KW	KW	pathological myopia; ocular histoplasmosis; pterygia; T1;	
KW	KW	punctate innerchorioidopathy; retinal degeneration; growth factor;	
KW	KW	vascularisation; vascular endothelial cell function; angiogenesis.	
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	WO200267970-A1.	
XX	XX		
PD	PD	06-SEP-2002.	
XX	XX		
PF	PF	22-FEB-2002; 2002WO-US005185.	
XX	XX		
PR	PR	23-FEB-2001; 2001US-0270951P.	
XX	XX		
PA	PA	(SCRI ) SCRIPPS RES INST.	
XX	XX		
PI	PI	Schimmel P, Wakasugi K, Friedlander M;	
XX	XX		
DR	DR	WPI; 2002-698635/75.	
XX	XX	N-PSDB; ABA00330.	
DR	DR		
PT	PT	New polypeptides derived from human tryptophanyl-tRNA synthase, useful	
PT	PT	for inhibiting ocular neovascularization in a patient, or for treating	
PT	PT	neovascular eye diseases, e.g. rubecotic glaucoma, retinopathy, keratitis,	
PT	PT	or pterygia.	
XX	XX		
PS	PS	Example 1; Page 71-72; 83pp; English.	
XX	XX		
CC	CC	This sequence represents a His6-tagged cleavage product, T1, of	
CC	CC	recombinant human tryptophanyl-tRNA synthase (TrpRS). A related cleavage	
CC	CC	product, T2, is water soluble and comprises residues 94-471 of full	
CC	CC	length TrpRS. The water-soluble T2 polypeptide is useful for inhibiting	
CC	CC	ocular neovascularisation in a patient. The T2 polypeptide is useful for	
CC	CC	treating neovascular eye diseases, e.g. age-related macular degeneration,	
CC	CC	ocular complications of diabetes, rubecotic glaucoma, retinopathy of	
CC	CC	prematurity, keratitis, ischaemic retinopathy (e.g. sickle cell),	

Db	62	FLRRGIFFSHRDNNQVLDAVENKPFYLYTGRGSPSSAMHVGHLIPFTFTKWLQDVFNVP	121
Qy	121	LVLTQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFFISDLIDYMGSSGFYKN	180
Db	122	LVLTQMTDDEKYLWKDLTLDQAYGDAVENAKDIACGFDINKTFFISDLIDYMGSSGFYKN	181
Qy	181	VVKIQKHVTNQVKGIFGFTSDCIGIKISPPAIOAAPSFSNSPFOIFRDRTDIOCLIFCA	240
Db	182	VVKIQKHVTNQVKGIFGFTSDCIGIKISFPPIAIOAAPSFSNSPFOIFRDRTDIOCLIFCA	241
Qy	241	IDQDPYFRMTRDVAPRIGYPKPAALLHSTFPPALOGAOTKMSASDPNSSIFLTDTAQIKT	300
Db	242	IDQDPYFRMTRDVAPRIGYPKPAALLHSTFPPALOGAOTKMSASDPNSSIFLTDTAQIKT	301
Qy	301	KVKAGHAFSGGRDTIEEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL	360
Db	302	KVKAGHAFSGGRDTIEEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL	361
Qy	361	KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSPDFQ	401
Db	362	KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSPDFQ	402
RESULT 4			
AAG79548			
ID AAG79548 standard; protein; 415 AA.			
XX	AC	AAG79548;	
XX	AC		
XX	XX		
DT	10-DEC-2002	(first entry)	
XX	XX		
XX	XX	His6-tagged TrpRS T1 polypeptide.	
KW	KW	T2; tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation;	
KW	KW	neovascular eye disease; age-related macular degeneration;	
KW	KW	ocular complication; diabetes; rubecotic glaucoma; retinopathy;	
KW	KW	prematurity; keratitis; ischaemic retinopathy; sickle cell;	
KW	KW	pathological myopia; ocular histoplasmosis; pterygia; T1;	
KW	KW	punctate innerchorioidopathy; retinal degeneration; growth factor;	
KW	KW	vascularisation; vascular endothelial cell function; angiogenesis.	
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	WO200267970-A1.	
XX	XX		
PD	PD	06-SEP-2002.	
XX	XX		
PF	PF	22-FEB-2002; 2002WO-US005185.	
XX	XX		
PR	PR	23-FEB-2001; 2001US-0270951P.	
XX	XX		
PA	PA	(SCRI ) SCRIPPS RES INST.	
XX	XX		
PI	PI	Schimmel P, Wakasugi K, Friedlander M;	
XX	XX		
DR	DR	WPI; 2002-698635/75.	
XX	XX	N-PSDB; ABA00330.	
DR	DR		
PT	PT	New polypeptides derived from human tryptophanyl-tRNA synthase, useful	
PT	PT	for inhibiting ocular neovascularization in a patient, or for treating	
PT	PT	neovascular eye diseases, e.g. rubecotic glaucoma, retinopathy, keratitis,	
PT	PT	or pterygia.	
XX	XX		
PS	PS	Example 1; Page 71-72; 83pp; English.	
XX	XX		
CC	CC	This sequence represents a His6-tagged cleavage product, T1, of	
CC	CC	recombinant human tryptophanyl-tRNA synthase (TrpRS). A related cleavage	
CC	CC	product, T2, is water soluble and comprises residues 94-471 of full	
CC	CC	length TrpRS. The water-soluble T2 polypeptide is useful for inhibiting	
CC	CC	ocular neovascularisation in a patient. The T2 polypeptide is useful for	
CC	CC	treating neovascular eye diseases, e.g. age-related macular degeneration,	
CC	CC	ocular complications of diabetes, rubecotic glaucoma, retinopathy of	
CC	CC	prematurity, keratitis, ischaemic retinopathy (e.g. sickle cell),	

CC pathological myopic, ocular histoplasmosis, pterygia, or punitate  
 CC innerchorioidopathy. This polypeptide is particularly useful for treating  
 CC retinal degeneration to prevent the damaging effects of trophic and  
 CC growth factors, and for promoting vascularisation to retard retinal  
 CC degeneration by enhancing blood flow to cells. These are also useful for  
 CC regulating vascular endothelial cell function, and in particular, for  
 CC inhibiting angiogenesis  
 XX  
 XX  
 SQ Sequence 415 AA;

Query Match 100.0%; Score 2116; DB 5; Length 415;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-209;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60  
 Db 2 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 61  
 Qy 61 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMVGHILPIFTKWLQDVNVP 120  
 Db 62 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMVGHILPIFTKWLQDVNVP 121  
 Qy 121 LVIQMTDDEKYLWKDLTLDAQYDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180  
 Db 122 LVIQMTDDEKYLWKDLTLDAQYDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 181  
 Qy 181 VVKIQKHVTFNQVKGIFGFTSDCGIKISFPAIQAPSFNSFPQIFRDRDTIOCLIPCA 240  
 Db 182 VVKIQKHVTFNQVKGIFGFTSDCGIKISFPAIQAPSFNSFPQIFRDRDTIOCLIPCA 241  
 Qy 241 IDQDPYFMRTRDVAPRIGYKPKALLHSTFFPALQAGQTKMSASDPNSIFLDTAKQIKT 300  
 Db 242 IDQDPYFMRTRDVAPRIGYKPKALLHSTFFPALQAGQTKMSASDPNSIFLDTAKQIKT 301  
 Qy 301 KVNKHAFIGSGGRDTTIEHRQFGNCNDVDSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 360  
 Db 302 KVNKHAFIGSGGRDTTIEHRQFGNCNDVDSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 361

## RESULT 5

ID ABU72386  
 XX ABU72386 standard; protein; 415 AA.

AC ABU72386;

DT 16-JUN-2003 (first entry)

DE Human supermini Tryptophanyl tRNA synthetase/His tag.

XX Human; tryptophanyl tRNA synthetase; TrpRS; angiogenesis; cytotstatic;  
 KW vulnary; Rossmann fold nucleotide binding domain; chemokine; EMAP II;  
 KW vascular endothelial cell; solid tumour; myocardial infarction; enzyme;  
 KW endothelial monocyte-activating polypeptide II; tumour metastasis;  
 KW wound healing; dermal ulcer; endothelialisation; vascular graft surgery;  
 KW abdominal wound; coronary bypass surgery; gene therapy.

XX Homo sapiens.

OS Synthetic.

XX US2002182666-A1.

XX 05-DEC-2002.

XX 21-MAR-2001; 2001US-00813718.

XX 21-MAR-2001; 2001US-00813718.

XX (SCHL/) SCHIMMEL P.

PA (WAKA/) WAKASUGI K.

Schimmel P, Wakasugi K;

WPI; 2003-340974/32.

N-PSDB; AC64107.

New truncated tryptophanyl-tRNA synthetase polypeptide comprising a  
 Rossmann fold nucleotide binding domain or having chemokine activity  
 useful for e.g. for regulating angiogenesis and for treating myocardial  
 infarction.

Example 1; Page 50-51; 9ipp; English.

The invention relates to an isolated polypeptide comprising a truncated  
 tryptophanyl-tRNA synthetase (TrpRS) polypeptide comprising a Rossmann  
 fold nucleotide binding domain or having chemokine activity. The isolated  
 polypeptide is capable of regulating vascular endothelial cell function.  
 TrpRS has a C-terminal domain containing an EMAP II (endothelial monocyte  
 -activating polypeptide II, a proinflammatory cytokine)-like domain and  
 is similar in sequence to TrpRS. Also included are a polynucleotide  
 encoding TrpRS (or a polynucleotide 95% similar to it) a TrpRS epitope,  
 5' and 3' deletions of the TrpRS polynucleotide, a recombinant vector  
 comprising an isolated TrpRS nucleic acid, a recombinant host cell  
 containing the TrpRS nucleic acid and expressing TrpRS, an isolated anti-  
 TrpRS antibody, producing truncations of TrpRS by treating it with a  
 protease, and suppressing angiogenesis, solid tumours or a condition that  
 would benefit from decreased angiogenesis in a mammal by administering to  
 the mammal the composition comprising the TrpRS truncated protein. The  
 isolated polypeptide is useful for the preparation of a pharmaceutical  
 composition for transdermal, transmucosal, enteral or parenteral  
 administration. The truncated tRNA synthetase polypeptide is useful for  
 research, diagnostic, prognostic and therapeutic applications. The tRNA  
 synthetase are useful for regulating vascular endothelial cell function,  
 particularly for regulating angiogenesis, for treating myocardial  
 infarction and solid tumour, and for suppressing tumour metastasis.  
 Angiogenic tRNA synthetase polypeptides are useful as wound healing  
 agents or for treating full thickness wounds such as dermal ulcers, in  
 the treatment of endothelialisation in vascular graft surgery, in the  
 treatment of abdominal wounds where there is a high risk infection, in  
 conjunction with coronary bypass surgery by stimulating the growth of the  
 transplanted tissue, and in gene therapy. The present sequence is a Trp  
 tRNA synthetase protein (full length, truncated or mutant) with a His  
 affinity tag

Sequence 415 AA;

Query Match 100.0%; Score 2116; DB 6; Length 415;

Best Local Similarity 100.0%; Pred. No. 1.7e-209;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60

Db 2 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 61

Qy 61 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMVGHILPIFTKWLQDVNVP 120

Db 62 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMVGHILPIFTKWLQDVNVP 121

Qy 121 LVIQMTDDEKYLWKDLTLDAQYDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180

Db 122 LVIQMTDDEKYLWKDLTLDAQYDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 181

Qy 181 VVKIQKHVTFNQVKGIFGFTSDCGIKISFPAIQAPSFNSFPQIFRDRDTIOCLIPCA 240

Db 182 VVKIQKHVTFNQVKGIFGFTSDCGIKISFPAIQAPSFNSFPQIFRDRDTIOCLIPCA 241

Qy 241 IDQDPYFMRTRDVAPRIGYKPKALLHSTFFPALQAGQTKMSASDPNSIFLDTAKQIKT 300

Db 242 IDQDPYFMRTRDVAPRIGYKPKALLHSTFFPALQAGQTKMSASDPNSIFLDTAKQIKT 301

Qy 301 KVNKHAFIGSGGRDTTIEHRQFGNCNDVDSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 360

Db 302 KVNKHAFIGSGGRDTTIEHRQFGNCNDVDSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 361

QY 361 KKALIEVLQPLIAHQARRKEVTDEIVKEFWTPRKLSFDFQ 401  
 ID AAB47616  
 DB 362 KKALIEVLQPLIAHQARRKEVTDEIVKEFWTPRKLSFDFQ 402

RESULT 6  
 AAB47616  
 ID AAB47616 standard; protein; 437 AA.  
 XX  
 AC AAB47616;  
 XX  
 DT 07-JAN-2002 (first entry)  
 XX  
 DE Human mini TrpRS.  
 XX  
 KW Tyrosyl-tRNA synthetase; TrpRS; Rosemann fold nucleotide binding domain;  
 KW vascular endothelial cell function; burn; plastic surgery; abdomen;  
 KW polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis;  
 KW angiogenesis; graft; myocardial infarction; solid tumour; wound healing;  
 KW dermal ulcer; diabetic ulcer; endothelialization;  
 KW typtophanyl-tRNA synthetase; trpRS; vascular graft surgery.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200174841-A1.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 21-MAR-2001; 2001WO-US008966.  
 XX  
 PR 31-MAR-2000; 2000US-0193471P.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Schimmel P, Wakasugi K;  
 XX  
 DR WPI; 2001-626377/72.  
 DR N-PSDB; AAH43603.  
 XX  
 PT New human truncated tyrosyl-tRNA synthetase polypeptide for regulating  
 PT vascular endothelial function, in particular for regulating angiogenesis,  
 PT tumor metastasis and treating myocardial infarction.  
 XX  
 PS Disclosure; Page 123-24; 150pp; English.  
 XX  
 CC The sequences given in AAB47615-18 show full length and truncated  
 CC versions of trptophanyl-tRNA synthetase (trpRS). The truncated trpRS of  
 CC the invention comprises a Rosemann fold nucleotide binding domain, and is  
 CC capable of regulating vascular endothelial cell function. It is of  
 CC approx. 40 kilo Dalton molecular weight and is produced by cleavage of  
 CC full length TrpRS with polymorphonuclear leucocyte elastase. Truncated  
 CC TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing  
 CC angiogenesis to a graft, treating myocardial infarction, solid tumor, and  
 CC a condition that would benefit from increased or decreased angiogenesis  
 CC in a mammal, in particular humans. It is also useful in diagnosis and as  
 CC a wound healing agent for treating wounds such as dermal ulcers, diabetic  
 CC ulcers, burns and injuries and in plastic surgery when reconstruction is  
 CC required following a burn or for cosmetic purposes. It is particularly  
 CC useful in the treatment of abdominal wounds where there is high risk of  
 CC infection. Truncated TrpRS promotes endothelialization in vascular graft  
 CC surgery and is used in conjunction with angiography to administer the  
 CC angiogenic tRNA synthetase polypeptides or polynucleotides directly to  
 CC the lumen and wall of the blood vessel  
 XX  
 SQ Sequence 437 AA;

Query Match 100.0%; Score 2116; DB 4; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-209;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNHGPDATAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 24 SNHGPDATAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 83  
 QY 61 FLRRGIFFSHRDNNQVLDAYENKKPFYLTGRGPFSEAMEHVGLHLPFIFTKWLQDVENVP 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 84 FLRRGIFFSHRDNNQVLDAYENKKPFYLTGRGPFSEAMEHVGLHLPFIFTKWLQDVENVP 143  
 QY 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTIFISDLDMGSSGGFYKN 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 144 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTIFISDLDMGSSGGFYKN 203  
 QY 181 VVKIQKHVTENOVKGIFGFTDSDICIGKISPPALQAAPSFNSPQIIFRDRDTIOCLIPCA 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 204 VVKIQKHVTENOVKGIFGFTDSDICIGKISPPALQAAPSFNSPQIIFRDRDTIOCLIPCA 263  
 QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTQMSASDPNSSIIFLDTAKOIKT 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 264 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTQMSASDPNSSIIFLDTAKOIKT 323  
 QY 301 KVNKHAFSGGRTIEHRQFGGNCVDVSPMYLTFFLEDDDDKLEQIRKQYTSGLMTGEL 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 324 KVNKHAFSGGRTIEHRQFGGNCVDVSPMYLTFFLEDDDDKLEQIRKQYTSGLMTGEL 383  
 QY 361 KKALIEVLQPLIAHQARRKEVTDEIVKEFWTPRKLSFDFQ 401  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 384 KKALIEVLQPLIAHQARRKEVTDEIVKEFWTPRKLSFDFQ 424

RESULT 7  
 AAE13492  
 ID AAE13492 standard; protein; 437 AA.  
 XX  
 AC AAE13492;  
 XX  
 DT 12-FEB-2002 (first entry)  
 XX  
 DE Human mini tryptophanyl t-RNA synthetase in pET20B.  
 XX  
 KW Human; tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA synthetase;  
 KW TyRS; vascular endothelial cell function; angiogenesis; wound healing;  
 KW re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury;  
 KW diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction;  
 KW angiography; gene therapy; tumour; inflammation; vascular permeability;  
 KW rheumatoid arthritis; psoriasis; diabetic retinopathy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175078-A1.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 21-MAR-2001; 2001WO-US008975.  
 XX  
 PR 31-MAR-2000; 2000US-0193471P.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Schimmel P, Wakasugi K;  
 XX  
 DR WPI; 2002-010784/01.  
 DR N-PSDB; AAD22483.  
 XX  
 PT Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of  
 PT regulating vascular endothelial cell function, preferably angiogenesis,  
 PT is useful for treating solid tumor or suppressing tumor metastasis in  
 PT mammal.  
 XX  
 PS Example 1; Page 123-124; 149pp; English.  
 XX  
 CC The patent discloses human aminoacyl tRNA synthetases, particularly  
 CC truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rosemann  
 CC fold nucleotide binding domain and polynucleotides encoding them. The  
 CC invention also relates to tyrosyl t-RNA synthetases (TyRS). TrpRS  
 CC sequences are useful for regulating vascular endothelial cell function,

CC preferably angiogenesis. Angiogenic TrpRS sequences are useful as wound  
 CC healing agents for re-vascularising damaged tissues. They are useful for  
 CC treating full-thickness wounds (e.g. dermal ulcers, including pressure  
 CC sores, venous ulcers and diabetic ulcers), burns and injuries. TrpRS  
 CC sequences can also be used in plastic surgery when reconstruction is  
 CC required following a burn, other trauma, or even for cosmetic purposes.  
 CC Angiogenic TrpRS is also used in association with surgery and following  
 CC the repair of cuts, for promoting endothelialisation in vascular graft  
 CC surgery and for repairing the damage of myocardial infarction and in  
 CC conjunction with coronary bypass surgery by stimulating the growth of  
 CC transplanted tissue. TrpRS is also used in conjunction with angiography.  
 CC TrpRS DNAs are useful in gene therapy. TrpRS antibodies are used in  
 CC immunoassays to detect the presence of tumours. They are also useful for  
 CC blocking endogenous angiogenic activity and retard the growth of solid  
 CC tumours. These antibodies may also be used to treat inflammation caused  
 CC by increased vascular permeability. Inhibiting the activity of TrpRS by  
 CC antisense technology is useful for preventing further growth or even  
 CC regress solid tumours, and for treating rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, all of which are characterised by abnormal  
 CC angiogenesis. The present sequence is human truncated tryptophanyl t-RNA  
 CC synthetase (mini TrpRS; residues 48-471 of full-length TrpRS protein)  
 CC protein in pET20B  
 CC  
 XX SQ Sequence 437 AA;

Query Match 100.0%; Score 2116; DB 5; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-209;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60  
 DB 24 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 83  
 QY 61 FLRRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTFKWLQDVNP 120  
 DB 84 FLRRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTFKWLQDVNP 143  
 QY 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTFFSDLDYMGSSGFYKN 180  
 DB 144 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTFFSDLDYMGSSGFYKN 203  
 QY 181 VVKIQKHVTFNQKIGFIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDTIOCLIPCA 240  
 DB 204 VVKIQKHVTFNQKIGFIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDTIOCLIPCA 263  
 QY 241 IDQDPYFRMTRDVA PRIGYPKALLHSTFFPALQAGTQKMSASDPNSIFLDTAKQIKT 300  
 DB 264 IDQDPYFRMTRDVA PRIGYPKALLHSTFFPALQAGTQKMSASDPNSIFLDTAKQIKT 323  
 QY 301 KVNKHAFFSGGRDTIEHRQFGNCNDVVSFMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 360  
 DB 324 KVNKHAFFSGGRDTIEHRQFGNCNDVVSFMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 383  
 QY 361 KALIEVLQPLIAEHQARKEVTDIVKFEFMTPRKLSDFQ 401  
 DB 384 KALIEVLQPLIAEHQARKEVTDIVKFEFMTPRKLSDFQ 424

## RESULT 8

AAG79547

ID AAG79547 standard; protein; 437 AA.

XX AC AAG79547;

XX DT 10-DEC-2002 (first entry)

XX DE His6-tagged mini-TrpRS polypeptide.

XX KW T2; tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation;

XX KW neovascular eye disease; age-related macular degeneration;

XX KW ocular complication; diabetes; rubecotic glaucoma; retinopathy;

XX KW prematurity; keratitis; ischaemic retinopathy; sickle cell;

XX KW pathological myopic; ocular histoplasmosis; pterygia;

KW puniate innerchorioidopathy; retinal degeneration; growth factor;  
 KW vascularisation; vascular endothelial cell function; angiogenesis.  
 XX Homo sapiens.  
 OS WO200267970-A1.  
 PN 06-SEP-2002.  
 PD 22-FEB-2002; 2002WO-US005185.  
 PF 23-FEB-2001; 2001US-0270951P.  
 XX (SCRI ) SCRIPPS RES INST.  
 PA Schimmel P, Wakaugi K, Friedlander M;  
 PI WPI; 2002-698635/75.  
 DR N-PSDB; ABA00329.  
 DR New polypeptides derived from human tryptophanyl-tRNA synthase, useful  
 XX for inhibiting ocular neovascularization in a patient, or for treating  
 XX neovascular eye diseases, e.g. rubecotic glaucoma, retinopathy, keratitis,  
 XX or pterygia.  
 XX Example 3; Fig 1; 83pp; English.

This sequence represents a His6-tagged cleavage product, mini-TrpRS, of  
 CC recombinant human tryptophanyl-tRNA synthase (TrpRS). A related cleavage  
 CC product, T2, is water soluble and comprises residues 94-471 of full  
 CC length TrpRS. The water-soluble T2 polypeptide is useful for inhibiting  
 CC ocular neovascularisation in a patient. The T2 polypeptide is useful for  
 CC treating neovascular eye diseases, e.g. age-related macular degeneration,  
 CC ocular complications of diabetes, rubecotic glaucoma, retinopathy of  
 CC prematurity, keratitis, ischaemic retinopathy (e.g. sickle cell),  
 CC pathological myopic, ocular histoplasmosis, pterygia, or puniate  
 CC innerchorioidopathy. This polypeptide is particularly useful for treating  
 CC retinal degeneration to prevent the damaging effects of trophic and  
 CC growth factors, and for promoting vascularisation to retard retinal  
 CC degeneration by enhancing blood flow to cells. These are also useful for  
 CC regulating vascular endothelial cell function, and in particular, for  
 CC inhibiting angiogenesis

Sequence 437 AA;

Query Match 100.0%; Score 2116; DB 5; Length 437;

Best Local Similarity 100.0%; Pred. No. 1.8e-209;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60  
 DB 24 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 83  
 QY 61 FLRRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTFKWLQDVNP 120  
 DB 84 FLRRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTFKWLQDVNP 143  
 QY 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTFFSDLDYMGSSGFYKN 180  
 DB 144 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTFFSDLDYMGSSGFYKN 203  
 QY 181 VVKIQKHVTFNQKIGFIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDTIOCLIPCA 240  
 DB 204 VVKIQKHVTFNQKIGFIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDTIOCLIPCA 263  
 QY 241 IDQDPYFRMTRDVA PRIGYPKALLHSTFFPALQAGTQKMSASDPNSIFLDTAKQIKT 300  
 DB 264 IDQDPYFRMTRDVA PRIGYPKALLHSTFFPALQAGTQKMSASDPNSIFLDTAKQIKT 323  
 QY 301 KVNKHAFFSGGRDTIEHRQFGNCNDVVSFMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 360  
 DB 324 KVNKHAFFSGGRDTIEHRQFGNCNDVVSFMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 383

QY 361 KKALIEVLQPLIAEHOARRKEVTDIEIVKFMTPRKLSFDQ 401  
 Db 384 KKALIEVLQPLIAEHOARRKEVTDIEIVKFMTPRKLSFDQ 424

## RESULT 9

ABU72385

ID ABU72385 standard; protein; 437 AA.

XX AC ABU72385;

XX DT

XX DT

XX DT 16-JUN-2003 (first entry)

XX DE

XX DE Human mini Tryptophanyl tRNA synthetase/His tag.

XX KW

XX KW Human; tryptophanyl tRNA synthetase; TrpRS; angiogenesis; cytostatic; vulnarary; Rossmann fold nucleotide binding domain; chemokine; EMAP II; vascular endothelial cell; solid tumour; myocardial infarction; enzyme; endothelial monocyte-activating polypeptide II; tumour metastasis; wound healing; dermal ulcer; endothelialisation; vascular graft surgery; abdominal wound; coronary bypass surgery; gene therapy.

XX OS

XX OS Homo sapiens.

XX OS Synthetic.

XX XX

XX PN US2002182666-A1.

XX XX

XX PD 05-DEC-2002.

XX XX

XX PF 21-MAR-2001; 2001US-00813718.

XX XX

XX PR 21-MAR-2001; 2001US-00813718.

XX XX

XX PA (SCHZ/) SCHIMMEL P.

XX PA (WAKA/) WAKASUGI K.

XX XX

XX PI Schimmel P, Wakasugi K;

XX XX

XX DR WPI; 2003-340974/32.

XX DR N-PSDB; ACA64106.

XX XX

PT New truncated tryptophanyl-tRNA synthetase polypeptide comprising a Rossmann fold nucleotide binding domain or having chemokine activity useful for e.g. for regulating angiogenesis and for treating myocardial infarction.

XX PS

XX PS Example 1; Page 46-47; 91pp; English.

XX CC

XX CC The invention relates to an isolated polypeptide comprising a truncated tryptophanyl-tRNA synthetase (TrpRS) polypeptide comprising a Rossmann fold nucleotide binding domain or having chemokine activity. The isolated polypeptide is capable of regulating vascular endothelial cell function. TrpRS has a C-terminal domain containing an EMAP II (endothelial monocyte-activating polypeptide II, a proinflammatory cytokine)-like domain and is similar in sequence to TrpRS. Also included are a polynucleotide encoding TrpRS (or a polynucleotide 95% similar to it) a TrpRS epitope, 5' and 3' deletions of the TrpRS polynucleotide, a recombinant vector comprising an isolated TrpRS nucleic acid, a recombinant host cell containing the TrpRS nucleic acid and expressing TrpRS, an isolated anti-TrpRS antibody, producing truncations of TrpRS by treating it with a protease, and suppressing angiogenesis, solid tumours or a condition that would benefit from decreased angiogenesis in a mammal by administering to the mammal the composition comprising the TrpRS truncated protein. The isolated polypeptide is useful for the preparation of a pharmaceutical composition for transdermal, transmucosal, enteral or parenteral administration. The truncated tRNA synthetase polypeptide is useful for research, diagnostic, prognostic and therapeutic applications. The tRNA synthetase are useful for regulating vascular endothelial cell function, particularly for regulating angiogenesis, for treating myocardial infarction and solid tumour, and for suppressing tumour metastasis. Angiogenic tRNA synthetase polypeptides are useful as wound healing agents or for treating full thickness wounds such as dermal ulcers, in the promotion of endothelialisation in vascular graft surgery, in the

CC treatment of abdominal wounds where there is a high risk infection, in conjunction with coronary bypass surgery by stimulating the growth of the CC transplanted tissue, and in gene therapy. The present sequence is a Trp CC tRNA synthetase protein (full length, truncated or mutant) with a His CC affinity tag  
 XX  
 SQ Sequence 437 AA;

Query Match 100.0%; Score 2116; DB 6; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-209;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60  
 Db 24 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 83  
 QY 61 FLRRGIFFFSHRDNNQVLDAYENKKPFYLYTGRGSPSEAMHVGHILIPFIFFKWLQDVNP 120  
 Db 84 FLRRGIFFFSHRDNNQVLDAYENKKPFYLYTGRGSPSEAMHVGHILIPFIFFKWLQDVNP 143  
 QY 121 LVIQMTDDEKYLWKOLTLDAQYGDVAENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180  
 Db 144 LVIQMTDDEKYLWKOLTLDAQYGDVAENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 203  
 QY 181 VKIQKHVTFNQVKGIFGFTSDSCIKISFPALQAAAPSFNSPQIFRDRDTIOCLIPCA 240  
 Db 204 VKIQKHVTFNQVKGIFGFTSDSCIKISFPALQAAAPSFNSPQIFRDRDTIOCLIPCA 263  
 QY 241 IDODPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTMSADPNSSIFLTDTAKOIKT 300  
 Db 264 IDODPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTMSADPNSSIFLTDTAKOIKT 323  
 QY 301 KVNKHAFFSGGRDTIEHRQFGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360  
 Db 324 KVNKHAFFSGGRDTIEHRQFGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 383  
 QY 361 KKALIEVLQPLIAEHOARRKEVTDIEIVKFMTPRKLSFDQ 401  
 Db 384 KKALIEVLQPLIAEHOARRKEVTDIEIVKFMTPRKLSFDQ 424

## RESULT 10

ADF76576

ID ADF76576 standard; protein; 471 AA.

XX AC

XX AC ADF76576;

XX DT

DT 26-FEB-2004 (first entry)

XX XX

XX DE Novel human secreted and transmembrane protein SeqID 250.

XX DE

XX KW human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.

XX OS

XX OS Homo sapiens.

XX PN

PN WO2003072035-A2.

XX XX

XX PD 04-SEP-2003.

XX XX

XX PF 21-FEB-2003; 2003WO-US005241.

XX XX

XX PR 22-FEB-2002; 2002US-0359461P.

XX XX

XX PA (GETH ) GENENTECH INC.

XX XX

XX PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;

XX PI Williams PM, Wood WI, Wu TD;

XX XX

XX DR WPI; 2003-721702/68.

DR N-PSDB; ADF76575.

XX New PRO polypeptides, useful for diagnosing and treating an immune

PT related disorder, e.g. systemic lupus erythematosus, rheumatoid

PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or

PT diabetes mellitus.

XX Claim 10; SEQ ID NO 250; 918pp; English.

XX This invention relates to novel nucleic acids encoding human PRO secreted

CC and transmembrane proteins. Extracellular proteins play important roles

CC in the formation, differentiation and maintenance of multicellular

CC organisms. The fate of many individual cells (for example proliferation,

CC migration or differentiation) is typically governed by information

CC received from other cells and the immediate environment. The information

CC is often transmitted by secreted polypeptides (for example mitogenic

CC factors, survival factors, cytotoxic factors, differentiation factors,

CC neuropeptides and hormones), which are received and interpreted by diverse

CC cell receptors or membrane bound proteins. These membrane bound proteins

CC and receptors may be of use as pharmaceutical and diagnostic agents, such

CC as in the blocking of receptor-ligand interactions. The current invention

CC provides the amino acid sequences of novel human membrane bound receptors

CC and proteins, along with the cDNA sequences encoding them. The novel

CC proteins of the invention may have cytosolic activities through the

CC stimulation of chondrocytes. The nucleic acids of the invention may be

CC useful for the manufacture of a medicament for diagnosing or treating a

CC tumour in a mammal. In addition, they may be useful for measuring or

CC detecting the expression of a tumour associated gene. The present

CC sequence is the amino acid sequence of a human PRO protein of the

CC invention.

XX SQ Sequence 471 AA;

Query Match 100.0%; Score 2116; DB 7; Length 471;

Best Local Similarity 100.0%; Pred. No. 2.1e-209;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 60

Db 71 SNHGPDTEAEEDFVDPWTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 130

Qy 61 FLRGIFPSHRDQVLDAYENKPFYLYTGRGSPSEAMHVGLIPIFTKWLQDVNP 120

Db 131 FLRGIFPSHRDQVLDAYENKPFYLYTGRGSPSEAMHVGLIPIFTKWLQDVNP 190

Qy 121 LVIQMTDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFISDLDYMGSSGFYKN 180

Db 191 LVIQMTDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFISDLDYMGSSGFYKN 250

Qy 181 VVKIQKHVTNQNKGIFGFTSDCIGKISFPALQAPSFNSFPQIFRDRDTIOCLIPCA 240

Db 251 VVKIQKHVTNQNKGIFGFTSDCIGKISFPALQAPSFNSFPQIFRDRDTIOCLIPCA 310

Qy 241 IDQDPYFRMTDVA PRIGYKPKALLHSTFFPALQQAOTKMSASDPNSISFLDTAKQIKT 300

Db 311 IDQDPYFRMTDVA PRIGYKPKALLHSTFFPALQQAOTKMSASDPNSISFLDTAKQIKT 370

Qy 301 KVNKHAFGSGRDTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 360

Db 371 KVNKHAFGSGRDTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 430

Qy 361 KKALIEVLQPLIAEHQAARKEVTDIVKEFMTPRKLSFDFQ 401

Db 431 KKALIEVLQPLIAEHQAARKEVTDIVKEFMTPRKLSFDFQ 471

RESULT 11

ABU64298

ID ABU64298 standard; protein; 471 AA.

XX AC ABU64298;

XX DT 11-MAR-2004 (first entry)

Human tryptophanyl-tRNA synthetase protein.

Vector; rAAV; recombinant adeno-associated viral vector;

anti-angiogenesis; PEDF; angiogenesis; eye disorder; blindness;

retinal degeneration; macular degeneration; neovascularisation;

ophthalmological.

Homo sapiens.

WO2003080648-A2.

02-OCT-2003.

20-MAR-2003; 2003WO-US008667.

20-MAR-2002; 2002US-0366114P.

(UYFL ) UNIV FLORIDA RES FOUND INC.

(UYUO ) UNIV JOHNS HOPKINS.

Hauswirth WW, Campochiaro PA, Berns KI;

WPI; 2003-779243/73.

N-PSDB; AAL56267.

Novel adeno-associated viral vector comprising polynucleotide encoding

pigment epithelium-derived factor, useful for treating choroidal

neovascularization, blindness, loss of vision.

Claim 14; Page 46; Opp; English.

The present invention relates to an adeno-associated viral (AAV) vector

comprising a polynucleotide that comprises a nucleic acid segment that

encodes a choroidal or ocular neovascularisation inhibitory polypeptide

operably linked to a promoter that expresses the segment to produce the

polypeptide in a selected mammalian host cell. Such a vector is useful

for providing a choroidal or ocular neovascularisation inhibitory

polypeptide to a mammal, for use in the therapy of ocular

neovascularisation, choroidal neovascularisation, retinal

neovascularisation, age-related macular degeneration, visual impairment,

ocular dysfunction, loss of vision, retinopathy, or blindness in a human.

The present sequence is a protein shown in the exemplification of the

invention

SQ Sequence 471 AA;

Query Match 100.0%; Score 2116; DB 7; Length 471;

Best Local Similarity 100.0%; Pred. No. 2.1e-209;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 60

Db 71 SNHGPDTEAEEDFVDPWTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 130

Qy 61 FLRGIFPSHRDQVLDAYENKPFYLYTGRGSPSEAMHVGLIPIFTKWLQDVNP 120

Db 131 FLRGIFPSHRDQVLDAYENKPFYLYTGRGSPSEAMHVGLIPIFTKWLQDVNP 190

Qy 121 LVIQMTDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFISDLDYMGSSGFYKN 180

Db 191 LVIQMTDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFISDLDYMGSSGFYKN 250

Qy 181 VVKIQKHVTNQNKGIFGFTSDCIGKISFPALQAPSFNSFPQIFRDRDTIOCLIPCA 240

Db 251 VVKIQKHVTNQNKGIFGFTSDCIGKISFPALQAPSFNSFPQIFRDRDTIOCLIPCA 310

Qy 241 IDQDPYFRMTDVA PRIGYKPKALLHSTFFPALQQAOTKMSASDPNSISFLDTAKQIKT 300

Db 311 IDQDPYFRMTDVA PRIGYKPKALLHSTFFPALQQAOTKMSASDPNSISFLDTAKQIKT 370

Qy 301 KVNKHAFGSGRDTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 360

Db 371 KVNKHAFGSGRDTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 430

Qy 361 KKALIEVLQPLIAEHQAARKEVTDIVKEFMTPRKLSFDFQ 401

Db 431 KKALIEVLQPLIAEHQAARKEVTDIVKEFMTPRKLSFDFQ 471



Db 371 KVNKHAFFSGGRDTEIEHRQFGGNCVDVSPFMYLTFFLEDDDDKLEQIRKDYTSGAMLTGEL 430

Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 401

Db 431 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 471

RESULT 12

ID ADN39916

ADN39916 standard; protein; 471 AA.

XX AC ADN39916;

XX DT 17-JUN-2004 (first entry)

XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C286.

XX DE

XX KW Human; differential expression; cancer; angiogenic disorder;

KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

KW inflammatory disease; autoimmune disease;

KW retinal neovascularisation syndrome; scarring; uterine fibroid;

KW detection; diagnosis; prognosis; drug screening; drug targeting;

KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;

XX KW vulnery; gene therapy; vaccine.

OS Homo sapiens.

XX PN WO2003042661-A2.

XX PD 22-MAY-2003.

XX PF 13-NOV-2002; 2002WO-US036810.

XX PR 13-NOV-2001; 2001US-0350666P.

PR 21-NOV-2001; 2001US-0332464P.

PR 29-NOV-2001; 2001US-0334393P.

PR 03-DEC-2001; 2001US-0335394P.

PR 14-DEC-2001; 2001US-0340376P.

PR 08-JAN-2002; 2002US-0347211P.

PR 10-JAN-2002; 2002US-0347349P.

PR 08-FEB-2002; 2002US-035250P.

PR 13-FEB-2002; 2002US-0356714P.

PR 20-FEB-2002; 2002US-0359077P.

PR 23-MAR-2002; 2002US-0368809P.

PR 04-APR-2002; 2002US-0370110P.

PR 12-APR-2002; 2002US-0372246P.

PR 05-JUN-2002; 2002US-0386614P.

PR 16-JUL-2002; 2002US-0396839P.

PR 22-JUL-2002; 2002US-0397775P.

PR 22-JUL-2002; 2002US-0397845P.

PR 09-SEP-2002; 2002US-0409450P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;

PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;

XX WPI; 2003-468649/44.

DR N-PSDB; ADN39699.

XX

PT Determining the presence or absence of a pathological cell in a patient,

PT useful for diagnosing, prognosing or treating cancer, comprises detecting

PT a nucleic acid in a biological sample.

XX

PS Claim 12; SEQ ID NO C286; 1385pp; English.

XX

CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

CC whose expression is upregulated or downregulated in specific cancers or

CC other diseases such as angiogenic or fibrotic disorders, and to methods

CC of determining the presence or absence of a pathological cell in a

CC patient by detecting a nucleic acid at least 80% identical to those of

CC the invention or by detecting a polypeptide of the invention. The

CC invention also relates to expression vectors and host cells comprising a

CC nucleic acid of the invention; antibodies which specifically bind a

CC polypeptide of the invention; use of such antibodies for drug targeting;

CC and methods of screening for modulators of activity or expression of the

CC polypeptides and nucleic acids. The nucleic acids, polypeptides,

CC antibodies and methods are useful for diagnosing, prognosing and treating

CC cancer and other conditions such as psoriasis, ischaemia, heart disease,

CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal

CC neovascularisation syndromes, scarring and uterine fibroids. They may

CC also be useful in wound healing and in contraception. The present

CC sequence represents a polypeptide of the invention.

XX

XX Sequence 471 AA;

Qy 1 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60

Db 71 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130

Qy 61 FLRGGIFFSHRDMNQVLDAYENKPFVLYTGRGSPSEAMHVGHLIPFIFTKWLQDVNP 120

Db 131 FLRGGIFFSHRDMNQVLDAYENKPFVLYTGRGSPSEAMHVGHLIPFIFTKWLQDVNP 190

Qy 121 LVIQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180

Db 191 LVIQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 250

Qy 181 VKIQKHVTFNQVKGIFGFTDSDICIKISPPAIQAAPSPNSPQIFRDRDTQCLIPCA 240

Db 251 VKIQKHVTFNQVKGIFGFTDSDICIKISPPAIQAAPSPNSPQIFRDRDTQCLIPCA 310

Qy 241 IDODPYFRMTRDVA PRIGYPKALLHSTFPALQGAQTQMSASDPNSSIFLTDTAKQIKT 300

Db 311 IDODPYFRMTRDVA PRIGYPKALLHSTFPALQGAQTQMSASDPNSSIFLTDTAKQIKT 370

Qy 301 KVNKHAFFSGGRDTEIEHRQFGGNCVDVSPFMYLTFFLEDDDDKLEQIRKDYTSGAMLTGEL 360

Db 371 KVNKHAFFSGGRDTEIEHRQFGGNCVDVSPFMYLTFFLEDDDDKLEQIRKDYTSGAMLTGEL 430

Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 401

Db 431 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 471

RESULT 13

ID ADJ75318 standard; protein; 471 AA.

XX AC ADJ75318;

XX DT 20-MAY-2004 (first entry)

XX DE

XX DE Marker gene related amino acid sequence SEQ ID NO:570.

XX KW bronchial asthma; chronic obstructive pulmonary disease;

KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;

KW gene therapy; marker.

XX OS Homo sapiens.

XX PN EP1394274-A2.

XX PD 03-MAR-2004.

XX 04-AUG-2003; 2003EP-00254857.

XX 06-AUG-2002; 2002JP-00229312.

XX 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.



QY 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSPQIFPRDRDTIOCLIPCA 240  
DB 251 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSPQIFPRDRDTIOCLIPCA 310  
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPFALQGAQTMSASDPNSSIFLTDTAKOIKT 300  
DB 311 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPFALQGAQTMSASDPNSSIFLTDTAKOIKT 370  
QY 301 KVNKHAFSGGRDTIEHRQFGGNCDDVSPMYLTFPLEDDDKLEQIRKDYTSGAMLTGEL 360  
DB 371 KVNKHAFSGGRDTIEHRQFGGNCDDVSPMYLTFPLEDDDKLEQIRKDYTSGAMLTGEL 430  
QY 361 KKALIEVLQPLIAEHOARRKEVTDEIVKEFMTPRKLSFDFQ 401  
DB 431 KKALIEVLQPLIAEHOARRKEVTDEIVKEFMTPRKLSFDFQ 471

RESULT 15  
AAB47615  
ID AAB47615 standard; protein; 484 AA.  
XX  
AC AAB47615;  
XX  
DT 07-JAN-2002 (first entry)  
XX  
DE Human full-length TrpRS.  
XX  
KW Tyrosyl-tRNA synthetase; TrpRS; Rosemann fold nucleotide binding domain;  
KW vascular endothelial cell function; burn; plastic surgery; abdomen;  
KW polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis;  
KW angiogenesis; graft; myocardial infarction; solid tumour; wound healing;  
KW dermal ulcer; diabetic ulcer; endothelialization;  
KW tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.  
XX  
OS Homo sapiens.  
XX  
PN WO200174841-A1.  
XX  
PD 11-OCT-2001.  
XX  
PF 21-MAR-2001; 2001WO-US008966.  
XX  
PR 31-MAR-2000; 2000US-0193471P.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Schimmel P, Wakaesugi K;  
XX  
XX  
DR WPI; 2001-626377/72.  
DR N-PSDB; AAH43602.  
XX  
XX New human truncated tyrosyl-tRNA synthetase polypeptide for regulating  
PT vascular endothelial function, in particular for regulating angiogenesis,  
PT tumor metastasis and treating myocardial infarction.  
XX  
PS Disclosure; Page 117-19; 150pp; English.  
XX  
XX The sequences given in AAB47615-18 show full length and truncated  
CC versions of tryptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of  
CC the invention comprises a Rosemann fold nucleotide binding domain, and is  
CC capable of regulating vascular endothelial cell function. It is of  
CC approx. 40 kilo Dalton molecular weight and is produced by cleavage of  
CC full length TrpRS with polymorphonuclear leucocyte elastase. Truncated  
CC TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing  
CC angiogenesis to a graft, treating myocardial infarction, solid tumor, and  
CC a condition that would benefit from increased or decreased angiogenesis  
CC in a mammal, in particular humans. It is also useful in diagnosis and as  
CC a wound healing agent for treating wounds such as dermal ulcers, diabetic  
CC ulcers, burns and injuries and in plastic surgery when reconstruction is  
CC required following a burn or for cosmetic purposes. It is particularly  
CC useful in the treatment of abdominal wounds where there is high risk of  
CC infection. Truncated TrpRS promotes endothelialization in vascular graft  
CC surgery and is used in conjunction with angiography to administer the

CC angiogenic tRNA synthetase polypeptides or polynucleotides directly to  
CC the lumen and wall of the blood vessel  
XX  
SQ Sequence 484 AA;  
Query Match 100.0%; Score 2116; DB 4; Length 484;  
Best Local Similarity 100.0%; Pred. No. 2.1e-209;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SNHGPDATAEEDFVDPWTQVTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP HH 60  
DB 71 SNHGPDATAEEDFVDPWTQVTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP HH 130  
QY 61 FLRRGIFFSHRDNQVLDAYENKKPFYLYTGRGPFSSSEAMHVGHLPFIPTKWLQDVFNVP 120  
DB 131 FLRRGIFFSHRDNQVLDAYENKKPFYLYTGRGPFSSSEAMHVGHLPFIPTKWLQDVFNVP 190  
QY 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTIFSDLDYMGHSSGPFYKN 180  
DB 191 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTIFSDLDYMGHSSGPFYKN 250  
QY 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSPQIFPRDRDTIOCLIPCA 240  
DB 251 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSPQIFPRDRDTIOCLIPCA 310  
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPFALQGAQTMSASDPNSSIFLTDTAKOIKT 300  
DB 311 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPFALQGAQTMSASDPNSSIFLTDTAKOIKT 370  
QY 301 KVNKHAFSGGRDTIEHRQFGGNCDDVSPMYLTFPLEDDDKLEQIRKDYTSGAMLTGEL 360  
DB 371 KVNKHAFSGGRDTIEHRQFGGNCDDVSPMYLTFPLEDDDKLEQIRKDYTSGAMLTGEL 430  
QY 361 KKALIEVLQPLIAEHOARRKEVTDEIVKEFMTPRKLSFDFQ 401  
DB 431 KKALIEVLQPLIAEHOARRKEVTDEIVKEFMTPRKLSFDFQ 471

Search completed: January 10, 2005, 21:19:43  
Job time : 157 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2005, 21:14:03 ; Search time 40 Seconds  
(without alignments)  
964.573 Million cell updates/sec

Title: US-09-813-718-10\_COPY\_71\_471  
Perfect score: 2116  
Sequence: 1 SNHGPDTEAEEDFVDPWTV.....VTDEIVKFWTPKLSFDFQ 401

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2101	99.3	471	1 A41706	tryptophan-tRNA li
2	2028.5	95.9	475	1 YWBO	tryptophan-tRNA li
3	1946.5	92.0	475	1 YWRBR	tryptophan-tRNA li
4	1938	91.6	481	2 S50053	tryptophan-tRNA li
5	1210	57.2	395	2 S58157	hypothetical prote
6	1163	55.0	432	2 S51901	tryptophan-tRNA li
7	907	42.9	386	2 C90190	tryptophanyl-tRNA
8	803	37.9	385	2 C75020	tryptophanyl-tRNA
9	626.5	29.6	301	2 G71206	tryptophan-tRNA li
10	534.5	25.3	380	2 G84372	tryptophanyl-tRNA
11	409.5	19.4	370	2 F64476	tryptophan-tRNA li
12	397.5	18.8	364	2 E69131	tryptophan-tRNA li
13	386	18.2	134	2 T43806	tryptophan-tRNA li
14	370.5	17.5	420	2 E69461	tryptophanyl-tRNA
15	353	16.7	374	2 D72477	probable tryptopha
16	269.5	12.7	513	2 F84373	tryptophanyl-tRNA
17	192	9.1	323	2 H69346	tyrosyl-tRNA synth
18	188	8.9	364	2 E72512	probable tyrosyl-t
19	185.5	8.8	341	2 D95260	tryptophanyl-tRNA
20	185.5	8.8	341	2 G98125	tryptophan-tRNA li
21	174.5	8.2	341	2 B86633	tryptophan-tRNA li
22	172	8.1	394	2 A45999	tyrosine-tRNA liga
23	170.5	8.1	366	2 S75410	tyrosine-tRNA liga
24	169	8.0	395	2 H70385	tryptophan-tRNA li
25	167	7.9	351	2 E75438	tryptophanyl-tRNA
26	166.5	7.9	346	2 B71496	tryptophan-tRNA li
27	164.5	7.8	895	2 A86410	protein F3M18.22 [
28	163.5	7.7	353	2 E70100	tryptophan-tRNA li
29	163	7.7	460	2 C84750	probable tyrosyl-t

RESULT 1

A41706

tryptophan-tRNA ligase (EC 6.1.1.2) [similarity] - human

N;Alternate names: interferon-inducible protein IFF53; peptide-chain release factor homo

C;Species: Homo sapiens (man)

C;Date: 19-May-2000 #sequence revision 19-May-2000 #text change 09-Jul-2004

C;Accession: A41633; A41706; S19246; JN0676; JH0533; S26287

R;Fleckner, J.; Rasmussen, H.H.; Justesen, J.

Proc. Natl. Acad. Sci. U.S.A. 88, 11520-11524, 1991

A;Title: Human interferon gamma protein induces the synthesis of a 55-kDa protein (gam

A;Reference number: A41633; MUID:92107982; PMID:1763065

A;Accession: A41633

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-471 <FLE>

A;Cross-references: UNIPROT:P23381; GB:X59892; NID:g30820; PIDN:CAA42545.1; PID:g30821

R;Rubin, B.Y.; Anderson, S.L.; King, L.; Powell, R.J.; Tate, W.P.

J. Biol. Chem. 266, 24245-24248, 1991

A;Title: Interferon induces tryptophanyl-tRNA synthetase expression in human fibroblasts

A;Reference number: A41706; MUID:92105071; PMID:1761529

A;Accession: A41706

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-471 <RUB>

A;Cross-references: GB:M77804; NID:g184656; PIDN:AAA67324.1; PID:g184657

R;Buwitt, U.; Flohr, T.; Boettger, E.C.

EMBO J. 11, 489-496, 1992

A;Title: Molecular cloning and characterization of an interferon induced human cDNA with

A;Reference number: S19246; MUID:92164636; PMID:1537332

A;Accession: S19246

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-423, 'R', 425-471 <BUN>

A;Cross-references: EMBL:X62570; NID:g32708; PIDN:CAA44450.1; PID:g32709

A;Note: 213-Ser and 214-Tyr were also found

R;Frolova, L.Y.; Grigorjeva, A.Y.; Sudomoina, M.A.; Kisselev, L.L.

Gene 128, 237-245, 1993

A;Title: The human gene encoding tryptophanyl-tRNA synthetase: Interferon-response eleme

A;Reference number: JN0676; MUID:93292992; PMID:7685728

A;Accession: JN0676

A;Molecule type: DNA

A;Residues: 1-141;182-471 <FPRO1>

A;Cross-references: GB:X67918; GB:S62837; NID:g37968; GB:X67919; NID:g37969; GB:X67920; GB:X6

4; NID:g37974; GB:X67925; GB:S62855; NID:g37975; GB:X67926; GB:S62856; NID:g37976; GB:X6

A;Note: the authors translated the codon GGG for residue 55 as Cys and GAG for residue 3

R;Frolova, L.Y.; Grigorjeva, A.Y.; Sudomoina, M.A.; Kisselev, L.L.

A;Note: this translation is not annotated in GenBank entries HSWRSX1A, HSWRSX2

Gene 109, 291-296, 1991

A;Title: Cloning and nucleotide sequence of the structural gene encoding for human trypt-

A;Reference number: JH0533; MUID:92112058; PMID:1765274

A;Accession: JH0533

A;Molecule type: mRNA

C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis  
F;24-69/Domain: amino acid-tRNA ligase repeat homology <ATL>

Query Match 95.9%; Score 2028.5; DB 1; Length 475;  
Best Local Similarity 95.8%; Pred. No. 4.6e-156; Indels 1; Gaps 1;  
Matches 384; Conservative 8; Mismatches 8;

QY 1 SNHGPDTEAEEDFVDPMTVTQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60  
DB 76 SEGLDATEADDFVDPMTVTQTSAGKIDYDKLIVRGSSKIDKELVNRIERATGQRP 135  
QY 61 FLRRGIFFSHRDMNQVLDAVENKPFYLYTGRGSSSEAMHVGHLPFFFTKWLQDV 120  
DB 136 FLRRGIFFSHRDMNQVLDAVENKPFYLYTGRGSSSEAMHVGHLPFFFTKWLQDV 195  
QY 121 LVQMTDDKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFY 180  
DB 196 LVQMTDDKYLWKDLTLDOAYGDAVENAKD-ITCGFDINKTFIFSDLDYMGSSGFY 254  
QY 181 VVKIQKHVTFNQVKGIFGFTSDCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIP 240  
DB 255 VVKIQKHVTFNQVKGIFGFTSDCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIP 314  
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSSIFLTD 300  
DB 315 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSSIFLTD 374  
QY 301 KVNKHAFSGGRDTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTS 360  
DB 375 KVNKHAFSGGRDTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTS 434  
QY 361 KXALIEVLQPLIAEHQARRKEVTDEIVKFMTPRKLSPDFQ 401  
DB 435 KXALIEVLQPLIAEHQARRKEVTDEIVKFMTPRKLSPDFQ 475

RESULT 3  
YWBO  
tryptophan-tRNA ligase (EC 6.1.1.2) [validated] - rabbit  
N;Alternate names: tryptophanyl-tRNA synthetase  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 30-Sep-1992 #sequence\_revision 13-Feb-1998 #text\_change 03-Jun-2002  
C;Accession: A35904; S37396  
R;Lee, C.C.; Craigen, W.J.; Muzny, D.M.; Harlow, E.; Caskey, C.T.  
A;Title: Cloning and expression of a mammalian peptide chain release factor with sequence  
A;Reference number: A35904; MUID:90239043; PMID:2185472  
A;Accession: A35904  
A;Molecule type: mRNA  
A;Residues: 1-475 <LSE>  
A;Cross-references: GB:M33460  
R;Frolova, L.Y.; Dalphin, M.E.; Justesen, J.; Powell, R.J.; Druegon, G.; McCaughan, K.K.;  
EMBO J. 12, 4013-4019, 1993  
A;Title: Mammalian polypeptide chain release factor and tryptophanyl-tRNA synthetase are  
A;Reference number: S37396; MUID:94009008; PMID:8404867  
A;Accession: S37396  
A;Molecule type: mRNA  
A;Residues: 166-177 <PRO>  
C;Genetics:  
A;Gene: WRS  
C;Complex: homodimer [validated, MUID:94009008]  
C;Function:  
A;Description: EC 6.1.1.2 [validated, MUID:94009008]; catalyzes the ATP-dependent format  
A;Note: mammalian WRS (tryptophanyl-tRNA synthetases) and eRF (polypeptide chain release  
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology  
C;Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; metalloprotein; protein  
F;23-68/Domain: amino acid-tRNA ligase repeat homology <Atl>  
F;174-177/Region: ATP-binding motif (HXGH)

Query Match 92.0%; Score 1946.5; DB 1; Length 475;  
Best Local Similarity 90.8%; Pred. No. 1.9e-149; Indels 1; Gaps 1;  
Matches 364; Conservative 21; Mismatches 15;

A;Residues: 1-212, 'GD', 215-471 <FRO2>  
A;Cross-references: GB:M61715; NID:G340367; PIDN:AAA61298.1; PID:G340368  
A;Experimental source: fibroblast  
C;Genetics:  
A;Gene: GDB:WARS; IFP53  
A;Cross-references: GDB:119632; OMIM:191050  
A;Map position: 14q23-14q31  
C;Introns: 33/3; 105/1; 141/2; 181/2; 242/2; 276/1; 313/3; 371/3; 418/3  
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology  
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis  
F;119-64/Domain: amino acid-tRNA ligase repeat homology <ATL>

Query Match 99.3%; Score 2101; DB 1; Length 471;  
Best Local Similarity 99.5%; Pred. No. 6.2e-162; Indels 0; Gaps 0;  
Matches 399; Conservative 0; Mismatches 2;

QY 1 SNHGPDTEAEEDFVDPMTVTQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60  
DB 71 SNHGPDTEAEEDFVDPMTVTQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 130  
QY 61 FLRRGIFFSHRDMNQVLDAVENKPFYLYTGRGSSSEAMHVGHLPFFFTKWLQDV 120  
DB 131 FLRRGIFFSHRDMNQVLDAVENKPFYLYTGRGSSSEAMHVGHLPFFFTKWLQDV 190  
QY 121 LVQMTDDKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFY 180  
DB 191 LVQMTDDKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFY 250  
QY 181 VVKIQKHVTFNQVKGIFGFTSDCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIP 240  
DB 251 VVKIQKHVTFNQVKGIFGFTSDCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIP 310  
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSSIFLTD 300  
DB 311 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSSIFLTD 370  
QY 301 KVNKHAFSGGRDTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTS 360  
DB 371 KVNKHAFSGGRDTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTS 430  
QY 361 KXALIEVLQPLIAEHQARRKEVTDEIVKFMTPRKLSPDFQ 401  
DB 431 KXALIEVLQPLIAEHQARRKEVTDEIVKFMTPRKLSPDFQ 471

RESULT 2  
YWBO  
tryptophan-tRNA ligase (EC 6.1.1.2) [validated] - bovine  
N;Alternate names: tryptophanyl-tRNA synthetase  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C;Accession: A40279; JN0354; S10450  
R;Garret, M.; Pajot, B.; Trezeguet, V.; Labouesse, J.; Merle, M.; Gandar, J.C.; Benedet  
Biochemistry 30, 7809-7817, 1991  
A;Title: A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic  
A;Reference number: A40279; MUID:91329348; PMID:1907847  
A;Accession: A40279  
A;Molecule type: mRNA  
A;Residues: 1-475 <GAR>  
A;Cross-references: UNIPROT:P17248; GB:M74074; EMBL:X53918; NID:G163798; PIDN:AAA30799.1  
A;Experimental source: pancreas  
A;Note: the authors translated the codon CTG for residue 347 as Ala and CAG for residue  
R;Zargarova, T.A.; Kovaleva, G.K.; Favorova, O.O.; Aevina, H.B.; Telezhinskaya, I.H.  
Bioorg. Khim. 15, 1307-1311, 1989  
A;Title: Amino acid sequence of several peptides of tryptophanyl-tRNA synthetase from ca  
A;Reference number: JN0354; MUID:90211408; PMID:2631684  
A;Accession: JN0354  
A;Molecule type: protein  
A;Residues: 112-124, 282-287, 'N', 288, 'F', 289-292, 'Q', 293-294, 'IR', 336-353, 423-441, 443-449  
A;Experimental source: liver  
A;Note: this paper is in Russian  
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology

[illegible]

C:Species: Mus musculus (house mouse)

```

RESULT 5
S58157
hypothetical protein SPAC2F7.13c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: S58157; T38561
R:Gentiles, S.; Churcher, C.M.
submitted to the EMBL Data Library, July 1995
A:Reference number: S58145
A:Accession: S58157
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <GEN>
A:Cross-references: UNIPROT:Q09692; EMBL:Z50142; NID:gl052783; PIDN:CAA90500.1;
R:Gentiles, S.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z21799
A:Accession: T38561
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-395 <GE2>
A:Cross-references: EMBL:Z50142; PIDN:CAA90500.1; GSPDB:GN00066; SPDB:SPAC2F7.1;
A:Experimental source: strain 972h-; cosmid c2F7
C:Genetics:
A:Gene: SPDB:SPAC2F7.13c
A:Map position: 1
C:Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat

Query Match 57.2%; Score 1210; DB 2; Length 395;
Best Local Similarity 59.6%; Pred. No. 5e-90;
Matches 235; Conservative 60; Mismatches 91; Indels 8; Gaps 4;

Qy 11 EEFVDPWTVQTS-----SAGIYDKLIIVRFGSSKIDKELINIERATGQRPHHFLRRGI 66
| | | | | : | | | | | : | | | | | : | | | | |
Db 4 EEQVTPWDVKGSIVDGEERKGIYERLIVQFGRKITPEQLERFEKLTGKKPHLLRRGA 63
| | | | | : | | | | | : | | | | | : | | | | |

Qy 67 FFSHRDMNVQLDAVENKKPPLYLTGRGPSSEAMHVGHLPFIETKMLQDVFNPLVLTQMT 126
| | | | | : | | | | | : | | | | | : | | | | |
Db 64 FFSHRQFDMLRDYEQKKPPLYLTGRGPSSDSMHLGHMIPFMFECKMLQDVQFVPLVLT 123
| | | | | : | | | | | : | | | | | : | | | | |

Qy 127 DDEKYLWKO-LTLDAQYGDVAENAKDIIACGFDPINKTFIFESDLDDYMGMSGGFYKNVVKIQ 165
| | | | | : | | | | | : | | | | | : | | | | |

```

QY 127 DDEKYLWKD-LTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFYKNVVKIQ 185





A;Experimental source: strain OT3  
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C;Genetics:  
A;Gene: PH1921  
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 29.6%; Score 626.5; DB 2; Length 301;  
Best Local Similarity 44.2%; Pred. No. 5e-43;  
Matches 134; Conservative 56; Mismatches 92; Indels 21; Gaps 7;

Qy 99 MHVGHLLPFTKWLQDVENVPLVIQMTDDEKYLWKD-LTLQAYGDVAVENAKDIITACGF 157  
Db 1 MHIGHIIPFATKWLQSKFGVNLVIQITDDEKFLKFNLTFTDTRKWAYDNILDIITAVGF 60  
Qy 158 DINKTFISDLIDYMGSSGFYKNVVKIQTHTFNVQVKGIFGTSDICIGKISFPFAIQAAP 217  
Db 61 DPDKTFIFQNSEF---TKIYEMAIPIAKINFSMAKAVFGFTEQSKIGMIFPFAIQIAP 116  
Qy 218 SFNSFFQIFRDRDIOCLIPCAIDQDPYFRWTRDVAPRIGYPKPAALLHSTTFPALQGAQ 277  
Db 117 TF-----FERK---RCLIPAAIDQDPYWLQDRFAESLGYGYKTAALHSKFVPSLTSL 166  
Qy 278 TKMSADPNSSIFLTDATAKIKTKVKNHAFSGGRDTIEHRQFGNCDVDVSPMYLTFFEL 337  
Db 167 GKMSASPEIAIYLTDSPEDEVKKWFTLTGGRTLKEQREKGEPEKCVFKWLEIFF 226  
Qy 338 EDDDKLRQIRKDY---TSGAMLTGELKKALIEVLQPLIAEHQARKEVDEIVKEFWTPR 394  
Db 227 EDDDK--KLKERYACKNGELTGCCKEYLSKIQEFLKEHQRRKK-AEKLVKPKYTG 293  
Qy 395 KLS 397  
Db 284 KLA 286

RESULT 10  
G84373  
tryptophanyl-tRNA synthetase [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: G84373  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;  
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: G84373  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-380 <STO>  
A;Cross-references: UNIPROT\_Q9HN66; GB:AE004437; NID:g10581646; PIDN:AAG20355.1; GSPDB:G1  
C;Genetics:  
A;Gene: trpS2  
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology

Query Match 25.3%; Score 534.5; DB 2; Length 380;  
Best Local Similarity 35.4%; Pred. No. 1.9e-35;  
Matches 141; Conservative 76; Mismatches 140; Indels 41; Gaps 17;

Qy 10 AEEDFVDPWTQTSAGIDYDKLIVRGSSKIDKELINRIERATGQRPHFLRRGIFFS 69  
Db 3 ADGNDVTPYAVESDD---LDYEKLARFGADELTDQARFP-----DHPLVNRGLFYA 53  
Qy 70 HRDMQVLDAYENKPPYLYTGRGPSSAMVGHILPIPIFTKWLQDVFNVLVIQMTDDE 129  
Db 54 GRDVDDFLTAGEQS---IVTGVGPGS-PHILGHAMVYFARRLQDEFGARVVVPLSDDE 108  
Qy 130 KYLWKDITLQOAYDAVE-NAKDIITACGFINDKTFIF---SPLDYM-GNSSGFYKNVVKI 184  
Db 109 KYWFKDQTPAET-GDYLRANLRDLAVGDFDELTRIVVDTRDADVLVPLATAPAGDV--- 164

```
QY 185 QKHVTFNQVKGIRGFTDSDICGKISPPAIAQAPSFNSFPQIFRDRDIOCLIPCAIDOD 244
Db 165 -RHATLQNVVG-----EPDNGVGAFFPAVQTAHL-----LPQLVHG--EHTLVPVIAVDQD 213

QY 245 PYFRMTRDVAPRIQY--KPALLHSTFPFALQAGTQMSASDPNSIFLTDTAQIKTKV 302
Db 214 PHVRSRDAVAKARYPVGKPGALLMQFLPSLAG-PGRWSSS-AGVSIRLTDSPDVTREKV 271

QY 303 NKHAFSGGRDTIEHHRQFGNCDDVDSFMYLTFFLEDD-KLQIRKDYTSGLMGTGLK 361
Db 272 RTHAYTGRASVEHRAKGVPAEDVPFQYLSAFPEFDDAELARIERYRAGLLSGELK 331

QY 362 KALIEVLQPLIAHQARKEVTDBIVKEFTPKLSPD 399
Db 332 DLAADRITFELAHQORRAALGD--VTEALDAFLRTDD 367

RESULT 11
F64476
Methanococcus jannaschii
N;Alternate names: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: F64476
R;Smith, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Bult, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rsen, J.D.; Sadov, P.W.; Hama, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: F64476
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-370 <BL>
A;Cross-references: UNIPROT:Q58810; GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99425.1;
C;Genetics:
A;Map position: FOR1375885-1376997
A;Start codon: GTG
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 19.4%; Score 409.5; DB 2; Length 370;
Best Local Similarity 30.9%; Pred. No. 2.3e-25;
Matches 119; Conservative 72; Mismatches 153; Indels 41; Gaps 16;

17 PWTQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQPHHPLRGIFFSHRDMMQV 76
8 PW--ETPAV--IDYKKTMEQGVKPIVDVLGDLKEE-----HHFFRNITLGHDFERI 57

QY 77 LDAYENKPFVLYTGRGSSAMHVGHLIPFTKWLQ---DVENVPLVIQMTDDEKYLW 133
Db 58 VDAIKNNKEFAVSGMPSGK-MHFGHKQVVDLKLKFKYQYTDNNIPI-----ADLEAYWA 112

QY 134 KDLTDAQYGDV-ENAKDIIACGPDINKTIFSDLDYMGSSGFYKNVVKI-QKHVTFN 191
Db 113 RNMSPFTKELALNEYITNYIALGLDPEKINVQLSKYQKV-----KDLALILSKRTNWS 167

QY 192 QVKGIFGTDSDCTGKISFPAAIAQAPSFNSFPQIFRDRT--DIQCLIPCAIDQPFPM 249
Db 168 EMKAIYGFKGTNIHVAFIVQVADIL---HPQLDENLSPPEPKPVVVPVGVIGDQPHRL 224

QY 250 TRDVAPR---IGYKPKALLHSTFPFALQAGTQMSASDPNSIFLTDTAQIKTKVAKHA 306
Db 225 TRDIANRAKEKFPITPSSYTHRFMTGLLG--KMSSKPEFAIFLTDDEKTVKKIFS-A 281

QY 307 FSGGRDTIEHHRQFGG---NCDVDVDSFMYLTFFLEDDDKLEQIRKDYTSGLMGTGLK 363
Db 282 KTGGRTELEHKKYGVPECVVYELFLY--HLILDKELAEIYQKCRSGBLTGCKCKM 339

QY 364 LIEVLQPLIAHQARKEVTDBIVK 388
Db 340 AYERVVEFLKDLKEKREQAKEIAVK 364
```

## RESULT 12

E69131

tryptophan-tRNA ligase (EC 6.1.1.2) - Methanobacterium thermoautotrophicum (strain Delta H)  
N;Alternate names: tryptophanyl-tRNA synthetase  
C;Species: Methanobacterium thermoautotrophicum  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: E69131  
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Qiu, D.; Spadator, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;  
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct:  
A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: E69131

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-364 <MTH>

A;Cross-references: UNIPROT:O26352; GB:AE000812; GB:AE000666; NID:g2621298; PIDN:AAB84751

A;Experimental source: strain Delta H

C;Genetics:

A;Gene: MTH251

A;Start codon: TTG

C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology

C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 18.8%; Score 397.5; DB 2; Length 364;

Best Local Similarity 27.9%; Pred. No. 2.1e-24;

Matches 107; Conservative 76; Mismatches 153; Indels 47; Gaps 14;

15 VDPWTQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQPHHPLRGIFFSHRDMM 74

2 IDPW----GSAK-LEYQDLIENFGVRPF-SEVLDE-----PEPSMLMRRGIIFGHRDYE 50

75 QVLDAYENKPFVLYTGRGSSAMHVGHLIPFTKWLQDVENVPLVIQMTDDEKYLW 134

51 RIISAMKKGEDFAVVTGMPPSGR-MHGHKQIVDQLRW-YDRMGAEIPIADIOMEAYSAR 108

135 DLATDAQYGDV-ENAKDIIACGPDINK-----TFISDLDYMGSSGFYKNVVK 183

109 GVPFESRRRIAEYTAGYIALGLDLEKONHIVYLOENLMVEDLAV----- 156

184 IQKHVTFNQVKGIFGTDSDCTGKISFPAAIAQAPSFNSFPQIFRDRDIOCLIPCAIDQ 243

157 LAGKWNFNELRAIYGTGTSMAHMAVAPIQVSDILHPQLDELGGPR---PVIVPVGPDQ 213

244 DPFRMTRDVAPRI---GYKPKALLHSTFPFALQAGTQMSASDPNSIFLTDTAQIK 299

214 DPHIRLTRDIAARFDRYGFILPSSTYHRFMGGLTGG--KQSSNRPKSAIFLSOTPEAE 271

300 TKVNGHAFSGGRDTIEHHRQFGNCDDVDSFMYLTFFLE-DDDKLEQIRKDYTSGLMGT 358

272 AKI-RNAKTGRTLEKQRELGGVPECIYETLLYHMGSDSRLEIYESCRNGTLMCG 330

359 ELKKALIEVLQPLIAEHQARKE 381

331 ECKNNTAEFIRKPFELSVMKREK 353

## RESULT 13

T43806

tryptophan-tRNA ligase (EC 6.1.1.2) [imported] - Encephalitozoon cuniculi (fragment)  
C;Species: Encephalitozoon cuniculi  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T43806

R;Peyrecaillade, E.; Brousseau, V.; Peyret, P.; Metenier, G.; Gouy, M.; Vivares, C.P.

Mol. Biol. Evol. 15, 683-689, 1998

A;Title: Microsporidia, amitochondrial protists, possess a 70-kDa heat shock protein gene

A;Reference number: 222693; MUID:98277683; PMID:9615449

A;Accession: T43806

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

Qy 311 RDTEEHQFGNCVDVSFMYLTFPLED-DDKLEQTKDYKDTSGAMLTGELKKALIEVLQ 369

Search completed: January 10, 2005, 21:23:46  
Job time : 42 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2005, 21:06:08 ; Search time 192 Seconds  
(without alignments)  
1201.694 Million cell updates/sec

Title: US-09-813-718-10\_COPY\_71\_471

Perfect score: 2116  
Sequence: 1 SNHGPDTEAEEDFVDPWTV.....VTDEIVKFWTPKLSDFDQ 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374546 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2101	99.3	471	1	SYW_HUMAN
2	2101	99.3	471	2	CAD62335
3	2028.5	95.9	475	1	SYW_BOVIN
4	1961.5	92.7	475	1	SYW_RABIT
5	1957	92.5	475	2	Q9DC65
6	1957	92.5	481	2	Q99J58
7	1953	92.3	475	2	Q80Z14
8	1938	91.6	481	1	SYW_MOUSE
9	1844	87.1	475	2	Q6NUA2
10	1844	87.1	475	2	AAH68695
11	1820	86.0	475	2	Q7ZWT7
12	1734	81.9	379	2	Q6P7B0
13	1734	81.9	379	2	AAH61752
14	1734	81.9	463	2	Q6PBS3
15	1734	81.9	463	2	AAH59603
16	1537	72.6	305	2	Q70184
17	1439.5	68.0	480	2	Q7Q9D2
18	1437.5	67.9	480	2	Q7Q9H6
19	1374.5	65.0	420	2	Q9UAY0
20	1374.5	65.0	430	2	Q9UAY1
21	1370.5	64.8	430	2	Q9VHG2
22	1323	62.5	417	2	Q9UIR2
23	1304	61.6	438	2	Q6CFA0
24	1301	61.5	402	2	Q9SR15
25	1210	57.2	395	1	SYW_SCHPO
26	1209	57.1	491	2	Q870U0
27	1180	55.8	425	2	Q6F0B6
28	1172	55.4	432	2	Q6CW15
29	1164.5	55.0	421	2	Q6B1L0
30	1163	55.0	432	1	SYWC_YEAST
31	1154.5	54.6	426	2	Q75A13

32 1154.5 54.6 426 2 AAS52037  
33 1026 48.5 632 2 Q8IDW3  
34 998 47.2 687 2 Q7RB96  
35 942 44.5 385 2 Q8SQV5  
36 916 43.3 429 2 Q8R0U7  
37 910.5 43.0 381 1 SYW\_SULTO  
38 905 42.8 380 1 SYW\_SULSO  
39 826.5 39.1 385 1 SYW\_PYRFU  
40 803 37.9 385 1 SYW\_PYRAB  
41 796 37.6 386 1 SYW\_PYRHO  
42 795.5 37.6 490 2 Q9UIF5  
43 735 34.7 375 1 SYW\_PYRAE  
44 701 33.1 377 2 Q74MK6  
45 701 33.1 377 2 AAR38970

#### ALIGNMENTS

RESULT 1  
SYW\_HUMAN  
ID SYW\_HUMAN STANDARD; PRT; 471 AA.  
AC P23381; P78535; Q9UDL3;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)  
DE (TrpRS) (IIPP53) (hWRS).  
GN Name=WARS;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92105071; PubMed=1761529;  
RA Rubin B.Y., Anderson S.L., Xing L., Powell R.J., Tate W.P.;  
RT "Interferon induces tryptophanyl-tRNA synthetase expression in human fibroblasts.";  
RL J. Biol. Chem. 266:24245-24248(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92107982; PubMed=1763065;  
RA Fleckner J., Rasmussen H.H., Justesen J.;  
RT "Human interferon gamma potentially induces the synthesis of a 55-kDa protein (gamma 2) highly homologous to rabbit peptide chain release factor and bovine tryptophanyl-tRNA synthetase.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:11520-11524(1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92112058; PubMed=1765274;  
RA Erolova L.Y., Sudomoina M.A., Grigorieva A.Y., Zinovieva O.L., Kisselev L.L.;  
RT "Cloning and nucleotide sequence of the structural gene encoding for human tryptophanyl-tRNA synthetase.";  
RL Gene 109:291-296(1991).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92164636; PubMed=1537332;  
RA Buwitt U., Fionr T., Boettger E.C.;  
RT "Molecular cloning and characterization of an interferon induced human cDNA with sequence homology to a mammalian peptide chain release factor.";  
RL EMBO J. 11:489-496(1992).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [6]  
RN SEQUENCE OF 1-13 FROM N.A.  
RX MEDLINE=96319994; PubMed=8724762;  
RA Sokolova I.V., Narovlianskii A.N., Amchenkova A.M., Turpaev K.T.;  
RT "Alternative splicing of 5'-terminal exons of the human tryptophanyl-  
RT tRNA synthetase gene";  
RL Mol. Biol. (Mosk.) 30:319-329 (1996).  
RN [7]  
RN SEQUENCE OF 1-141 AND 182-471 FROM N.A.  
RC TISSUE=Sperm;  
RA MEDLINE=93292992; PubMed=7685728;  
RX Frolova L.Y., Grigorieva A.Y., Sudomoina M.A., Kiselev L.L.;  
RT "The human gene encoding tryptophanyl-tRNA synthetase: interferon-  
RT response elements and exon-intron organization.";  
RL Gene 128:237-245 (1993).  
RN [8]  
RN SEQUENCE OF 265-276; 278-296; 299-317 AND 350-365.  
RC TISSUE=Keratinocytes;  
RX MEDLINE=93162043; PubMed=1286667;  
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.B.,  
RA Vandekerckhove J.;  
RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
RT protein database of normal human epidermal keratinocytes.";  
RL Electrophoresis 13:960-969 (1992).  
RN [9]  
RN FUNCTION.  
RX MEDLINE=9225128; PubMed=1373391;  
RA Bange F.-C., Florh T., Buwitt U., Boettger B.C.;  
RT "An interferon-induced protein with release factor activity is a  
RT tryptophanyl-tRNA synthetase";  
RL FEBS Lett. 300:162-166 (1992).  
CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +  
CC diphosphate + L-tryptophanyl-tRNA(Trp).  
CC -1- SUBUNIT: Homodimer.  
CC -1- INDUCTION: By interferon gamma.  
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.  
CC -1- SIMILARITY: Contains 1 WHEP-TRS domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M77804; AAA67324.1; -;  
CC EMBL; X59892; CAA42545.1; -;  
CC EMBL; M61715; AAA61298.1; -;  
CC EMBL; X62570; CAA44501.1; -;  
CC EMBL; BC017489; AAA17489.1; -;  
CC EMBL; S82905; AAB39381.1; -;  
CC EMBL; X67920; CAB94198.1; -;  
CC EMBL; X67921; CAB94198.1; JOINED.  
CC EMBL; X67922; CAB94198.1; JOINED.  
CC EMBL; X67923; CAB94199.1; -;  
CC EMBL; X67924; CAB94199.1; JOINED.  
CC EMBL; X67925; CAB94199.1; JOINED.

DR EMBL; X67926; CAB94199.1; JOINED.  
DR EMBL; X67927; CAB94199.1; JOINED.  
DR EMBL; X67928; CAB94199.1; JOINED.  
DR PR; A41633; A41706.  
DR PDB; 1R6T; X-ray; A/B=1-471.  
DR PDB; 1R6U; X-ray; A/B=48-471.  
DR PDB; 1ULH; X-ray; A/B=82-471.  
DR Aarhus/Ghent-2DPAGE; 3524; IEF.  
DR OGP; P23381; -;  
DR PHCI-2DPAGE; P23381; -;  
DR Genew; HGNC:12729; WARS.  
DR MM; 191050; -;  
DR GO; GO:0005737; C:cytoplasm; TAS.  
DR GO; GO:0005625; C:soluble fraction; TAS.  
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.  
DR GO; GO:0006412; P:protein biosynthesis; TAS.  
DR GO; GO:0006436; P:tryptophanyl-tRNA aminoacylation; TAS.  
DR InterPro; IPR009068; S15/NS1 bind.  
DR InterPro; IPR002305; tRNA-synt\_1b.  
DR InterPro; IPR001412; tRNA-synt\_1.  
DR InterPro; IPR002306; Trp tRNA-synt\_1b.  
DR InterPro; IPR000738; WHEP-TRS.  
DR Pfam; PF00579; tRNA-synt\_1b; 1.  
DR Pfam; PF00458; WHEP-TRS; 1.  
DR PRINTS; PRO1039; TRNASYNTHTRP.  
DR TIGRFAMS; TIGR00233; trps; 1.  
DR PROSITE; PS00178; AA tRNA LIGASE I; 1.  
DR PROSITE; PS00762; WHEP-TRS; 1.  
KW 3D-structure; Aminoacyl-tRNA synthetase; ATP-binding;  
KW Direct protein sequencing; Ligase; Protein biosynthesis.  
FT DOMAIN 19 64  
FT SITE 164 173 "HIGH" region.  
FT SITE 349 353 "KMSKS" region.  
FT CONFLICT 213 214 SY -> GD (in Ref. 3).  
FT CONFLICT 424 424 A -> R (in Ref. 4).  
SQ SEQUENCE 471 AA; 53165 MW; E9634444903JA0D0 CRC64;  
Query Match 99.3%; Score 2101; DB 1; Length 471;  
Best Local Similarity 99.5%; Pred. No. 5.4e-160;  
Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 SNHGPDTEAEEDFVDPWTVTQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 60  
Db 71 SNHGPDTEAEEDFVDPWTVTQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 130  
Qy 61 FLRGIFFSHRDMQVLDAYENKKPFYLYTGRGSPSEAMHVGLIPIFTKWLQDVNP 120  
Db 131 FLRGIFFSHRDMQVLDAYENKKPFYLYTGRGSPSEAMHVGLIPIFTKWLQDVNP 190  
Qy 121 LVIQMTDDEKYLWKDLTDOAYGDAVENAKDIIACGPDINKTFFSDLDYGMSSGFYKN 180  
Db 191 LVIQMTDDEKYLWKDLTDOAYGDAVENAKDIIACGPDINKTFFSDLDYGMSSGFYKN 250  
Qy 181 WKIQKHVTNQVKGIFGFTSDICIGKISPAQAAPSFNSPQIFRDRDITDCLIPCA 240  
Db 251 WKIQKHVTNQVKGIFGFTSDICIGKISPAQAAPSFNSPQIFRDRDITDCLIPCA 310  
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKI 300  
Db 311 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKI 370  
Qy 301 KVNKHAFFSGGRDTIEHRQFGNGCDVDVSPMYLTFPLEDDOKLEIQIRKDYTSGLMTGEL 360  
Db 371 KVNKHAFFSGGRDTIEHRQFGNGCDVDVSPMYLTFPLEDDOKLEIQIRKDYTSGLMTGEL 430  
Qy 361 KCALEIVLQPLIAEHQARRKEVTDEIVKEFWTPKLSFDFQ 401  
Db 431 KCALEIVLQPLIAEHQARRKEVTDEIVKEFWTPKLSFDFQ 471  
RESULT 2  
CAD62335  
ID CAD62335 PRELIMINARY; PRT; 471 AA.

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AC CAD62335;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Human full-length cDNA clone CS0DM004VH09 of Fetal liver of Homo
DE sapiens (human).
OS Homo sapiens (human).
OG Plasmid pcMVSPORT_6.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RA Genoscope;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RA "Full-length cDNA libraries and normalization.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX248006; CAD62335.1; -.
KW Plasmid
SQ SEQUENCE 471 AA; 53165 MW; E96344449053A0D0 CRC64;

Query Match 99.3%; Score 2101; DB 2; Length 471;
Best Local Similarity 99.5%; Pred. No. 5.4e-160;
Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNHGPDATAEEDFVDPWTVTQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
DB 71 SNHGPDATAEEDFVDPWTVTQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 130
QY 61 FLRRGIFFSHRDQNVLDAYENKKPFYLTGRGSSSEAMHVGLIPFIPTKWLQDVFNVP 120
DB 131 FLRRGIFFSHRDQNVLDAYENKKPFYLTGRGSSSEAMHVGLIPFIPTKWLQDVFNVP 190
QY 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180
DB 191 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 250
QY 181 VKIQKHVTNQVKGIFGFTSDICIGKISPPAIOAAPSFNSFPQIPRDRDTQCLIPCA 240
DB 251 VKIQKHVTNQVKGIFGFTSDICIGKISPPAIOAAPSFNSFPQIPRDRDTQCLIPCA 310
QY 241 IDQDPYFRMTRDVPAPRIGYKPKALLHSTFPALQGAQTKMSADPNSSIFELDTAKQIKT 300
DB 311 IDQDPYFRMTRDVPAPRIGYKPKALLHSTFPALQGAQTKMSADPNSSIFELDTAKQIKT 370
QY 301 KVNKHAFFSGGRDITIEHRQFGNCDVDVSPMYLTFFLEDDDKLEQIRKDYTGAMLTGEL 360
DB 371 KVNKHAFFSGGRDITIEHRQFGNCDVDVSPMYLTFFLEDDDKLEQIRKDYTGAMLTGEL 430
QY 361 KKALIEVLQPLIAHQARRKEVTDEIVKEFWTPRKLSFDFQ 401
DB 431 KKALIEVLQPLIAHQARRKEVTDEIVKEFWTPRKLSFDFQ 471

RESULT 3
SYW BOVIN
ID AC PL7248;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
DE (TrpRS).
GN Name=WARS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=91329348; PubMed=1907847;
RA Garret M., Pajot B., Trezeguet V., Labouesse J., Merle M.,
RA Gandar J.-C., Benedetto J.-P., Salliafranke M.-L., Alterio J.,
RA Gueguen M., Sarger C., Labouesse B., Bonnet J.;
RA "A mammalian tryptophanyl-tRNA synthetase shows little homology to
RT prokaryotic synthetases but near identity with mammalian peptide chain
RT release factor.";
RL Biochemistry 30:7809-7817(1991).
RN [2]
RP SEQUENCE OF 17-475 FROM N.A.
RC TISSUE=Pancreas;
RA Garret M., Trezeguet V., Pajot B., Gandar J.-C., Merle M.,
RA Gueguen M., Benedetto J.-P., Sarger C., Alterio J., la Boussec B.,
RA Labouesse J., Bonnet J.;
RL Submitted (MAR-1990) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
CC diphosphate + L-tryptophanyl-tRNA(Trp).
CC -I- SUBUNIT: Homodimer.
CC -I- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -I- SIMILARITY: Contains 1 WHEP-TRS domain.
CC
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CC
CC EMBL: X53918; CAA37872.1; -.
CC EMBL: X52113; CAA36356.1; -.
CC PIR: A0279; YWEO.
CC HSP: P07814; IFYD.
CC InterPro: IPR009068; S15/NSI_bind.
CC InterPro: IPR002305; tRNA-synt_1b.
CC InterPro: IPR001412; tRNA-synt_1.
CC InterPro: IPR002306; Trp tRNA-synt_1b.
CC InterPro: IPR000738; WHEP-TRS.
CC Pfam: PF00579; tRNA-synt_1b; 1.
CC Pfam: PF00458; WHEP-TRS; 1.
CC PRINTS: PR01039; TRNASYNTHTRP.
CC TIGRFAMs: TIGR00233; trps; 1.
CC PROSITE: PS00178; AA tRNA LIGASE_I; 1.
CC PROSITE: PS00762; WHEP-TRS; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Direct protein sequencing;
KW Ligase; Protein biosynthesis.
KW DOMAIN 24 69 WHEP-TRS.
FT DOMAIN 1 117 DISPENSABLE TO THE CATALYTIC ACTIVITY.
FT SITE 169 178 "HIGH" region.
FT SITE 353 357 "KMSKS" region.
FT CONFLICT 17 17 L -> M (in Ref. 2).
SQ SEQUENCE 475 AA; 53729 MW; F7E531750137EB32 CRC64;

Query Match 95.9%; Score 2028.5; DB 1; Length 475;
Best Local Similarity 95.8%; Pred. No. 3.6e-154;
Matches 384; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 SNHGPDATAEEDFVDPWTVTQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
DB 76 SGEGLDATAEEDFVDPWTVTQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 135
QY 61 FLRRGIFFSHRDQNVLDAYENKKPFYLTGRGSSSEAMHVGLIPFIPTKWLQDVFNVP 120
DB 136 FLRRGIFFSHRDQNVLDAYENKKPFYLTGRGSSSEAMHVGLIPFIPTKWLQDVFNVP 195
QY 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180
DB 196 LVQMTDDEKYLWKDLTLDOAYGDAVENAKD-ITCGFDINKTIFSDLDYMGSSGFYKN 254
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QY 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPAIAQAAPSFNSPFIQIRDRDIOCLIPCA 240
Db 255 VVKIQHVTNQVKGIFGFTSDSCIGKISPAIAQAAPSFNSPFIQIRDRDIOCLIPCA 314
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAOTKMSADPNSSIFLTDTAKOIKT 300
Db 315 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAOTKMSADPNSSIFLTDTAKOIKT 374
QY 301 KVNKHAFSGGRDTEEHRRQFGGNCDDVSPMYLTFLEDDDKLEIQIRKDYTSGAMLGTGEL 360
Db 375 KVNKHAFSGGRDTEEHRRQFGGNCDDVSPMYLTFLEDDDKLEIQIRDYSGNMLGTGEL 434
QY 361 KKALIEVLQPLIAEHQARRKEVTDIVKEFWTPRKLSFDQ 401
Db 435 KKALIEVLQPLIAEHQARRKEVTDIVKEFWTPRKLSFDQ 475

RESULT 4
SYW RABBIT STANDARD; PRT; 475 AA.
AC P23612; Q28607;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
DE (TrpRS).
GN Name=WARS;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90239043; PubMed=2185472;
RA Lee C.C., Craigm W.J., Muzny D.M., Harlow E., Caskey C.T.;
RT "Cloning and expression of a mammalian peptide chain release factor
with sequence similarity to tryptophanyl-tRNA synthetases.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3508-3512(1990).
RN [2]
RP REVISIONS TO 169-174 AND 227-228, AND FUNCTION.
RX MEDLINE=94009008; PubMed=8404867;
RA Frolova L.Y., Dalphin M.E., Justesen J., Powell R.J., Drugeon G.,
RA McCaughan K.K., Kiselev L.L., Tate W.P., Haenni A.-L.;
RT "Mammalian polypeptide chain release factor and tryptophanyl-tRNA
synthetase are distinct proteins.";
RL EMBO J. 12:4013-4019(1993).
CC -I- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
diphosphate + L-tryptophanyl-tRNA(Trp).
CC -I- SUBUNIT: Homodimer (By similarity).
CC -I- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -I- SIMILARITY: Contains 1 WHEP-TRS domain.
CC -I- CAUTION: Was originally (Ref.1) thought to be a eukaryotic release
factor (ERF).
CC
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or send an email to license@sib-sib.ch).
CC
CC -----
CC ENBL; M33460; AAA31246.1; ALT_SEQ.
DR ENBL; U02595; AAB60257.1; -.
DR HSP; P07814; IRYJ.
DR InterPro; IPR009068; S15/NS1_bind.
DR InterPro; IPR002305; tRNA-synt_1b.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002306; Trp tRNA-synt_1b.
DR InterPro; IPR000738; WHEP-TRS.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR Pfam; PF00458; WHEP-TRS; 1.
DR PRINTS; PRO1039; TRNASYNTHTRP.

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DR TIGRFAMS; TIGR00233; trpS; 1.
DR PROSITE; PS00178; AA TRNA LIGASE I; 1.
DR PROSITE; PS00762; WHEP TRS; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis.
FT DOMAIN 23 68 WHEP-TRS
FT SITE 168 177 "HIGH" region.
FT SITE 353 357 "KMSKS" region.
SQ SEQUENCE 475 AA; 53799 MW; 33BC9E718FF45DC4 CRC64;

Query Match 92.7%; Score 1961.5; DB 1; Length 475;
Best Local Similarity 91.5%; Pred No. 8.6e-149;
Matches 367; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

QY 2 NHG-PDATEAEEDFVDPWTQTSSAKGIDYDKLIVRFSGSSKIDKELINRIERATGQRP HH 60
Db 75 SHGDPEAVDDKEDFVDPWTVRTSSAKGIDYDKLIVFGSSKIDKELVNIERATGQRP HR 134
QY 61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGFSSEAMHVGHLLPIFTKWLQDVNPV 120
Db 135 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGFSSEAMHVGHLLPIFTKWLQDVNPV 194
QY 121 LVIQMTDDKYLWKDLTLDOAYGDVADENAKDIITACGFDINKTIFESLDLYMGSSGFGYKN 180
Db 195 LVQMSDDKYLWKDLTLQVYGYTLENAKDIITACGFDVKNKTFISLDLYMGSSGFGYKN 254
QY 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPAIAQAAPSFNSPFIQIRDRDIOCLIPCA 240
Db 255 VVKIQHVTNQVKGIFGFTSDSCIGKISPAIAQAAPSFNSPFIQIRDRDIOCLIPCA 314
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAOTKMSADPNSSIFLTDTAKOIKT 300
Db 315 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAOTKMSADPNSSIFLTDTAKOIKT 374
QY 301 KVNKHAFSGGRDTEEHRRQFGGNCDDVSPMYLTFLEDDDKLEIQIRKDYTSGAMLGTGEL 360
Db 375 KVNKHAFSGGRDTEEHRRQFGGNCDDVSPMYLTFLEDDDKLEIQIRKDYSGAMLGTGEL 434
QY 361 KKALIEVLQPLIAEHQARRKEVTDIVKEFWTPRKLSFDQ 401
Db 435 KKALIEVLQPLIAEHQARRKEVTDIVKEFWTPRKLSFDQ 475

RESULT 5
Q9DC65 PRELIMINARY; PRT; 475 AA.
ID AC Q9DC65;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200002C07 product:tryptophanyl-tRNA synthetase, full insert
sequence.
GN Name=Wars;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.

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DR InterPro; IPR002305; tRNA-synt 1b.  
 DR InterPro; IPR001412; tRNA-synt 1.  
 DR InterPro; IPR002306; Trp tRNA-synt 1b.  
 DR InterPro; IPR000738; WHEP-TRS.  
 DR Pfam; PF00579; tRNA-synt 1b; 1.  
 DR Pfam; PF00458; WHEP-TRS; 1.  
 DR PRINTS; PR01039; TRNASYNTHTRP.  
 DR TIGRFAMs; TIGR00233; trps; 1.  
 DR PROSITE; PS00178; AA TRNA LIGASE I; 1.  
 DR PROSITE; PS00762; WHEP-TRS; 1.  
 KW Aminoacyl-tRNA synthetase.  
 SQ SEQUENCE 481 AA; 54325 MW; A754E1DDPF58E2EF3 CRC64;

Query Match 92.5%; Score 1957; DB 2; Length 481;  
 Best Local Similarity 91.5%; Pred. No. 2e-148;  
 Matches 366; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 2 NHGPDATAEEDFVDPWMTVOTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRPHHF 61  
 DB 76 NCSDATKASEDFVDPWMTVOTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRPHF 135

QY 62 LRGGIFSHRDMNQVLDAVENKPPFYLTYGRGSPSEAMHGLHPFFFTKWLQDVFNPL 121  
 DB 136 LRGGIFSHRDMNQVLDAVENKPPFYLTYGRGSPSEAMHGLHPFFFTKWLQDVFNPL 195

QY 122 VIQWTDDEKYLWKDLTLDDQAYGDAVENAKDIIACGPDINKTFIFSDLDYMGSSGFYKNV 181  
 DB 196 VIQMSDDEKYLWKDLTLDDQAYSYTVENAKDIIACGPDINKTFIFSDLEYMGQSPGFYRNV 255

QY 182 VKIQKHVTFNQVKGIFGTFDSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCAI 241  
 DB 256 VKIQKHVTFNQVKGIFGTFDSDCIGKISFPAVQAQPSFNSFPKIFRDRDIOCLIPCAI 315

QY 242 DQDPYFMTDRDVPRIQVPRIGYKPKALLHSTFFPALQAGTQMSASDPNSSIFLDTAKQIKTK 301  
 DB 316 DQDPYFMTDRDVPRIQVPRIGYKPKALLHSTFFPALQAGTQMSASDPNSSIFLDTAKQIKSK 375

QY 302 VNKHAFSGGRDTIEHRQFGNCVDVDSFMYLTFFLEDDDKLEQIRKDYTSGLMTGELK 361  
 DB 376 VNKHAFSGGRDTIEHRQFGNCVDVDSFMYLTFFLEDDDLRLQIRKDYTSGLMTGELK 435

RESULT 7  
 Q80ZY4 PRELIMINARY; PRT; 475 AA.

AC Q80ZY4;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Wars protein.  
 GN Name=Wars;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smaluk D.E., Schmerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC046232; AAH46232.1; -.  
 DR HSSP; P07814; IFYJ.  
 DR MGD; MGI:104630; Wars.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004830; P:tryptophan-tRNA ligase activity; IEA.  
 DR GO; GO:0006436; P:tryptophanyl-tRNA aminoacylation; IEA.  
 DR InterPro; IPR009068; S15/NS1 bind.  
 DR InterPro; IPR002305; tRNA-synt 1b.  
 DR InterPro; IPR001412; tRNA-synt 1.  
 DR InterPro; IPR002306; Trp tRNA-synt 1b.  
 DR Pfam; PF00579; tRNA-synt 1b; 1.  
 DR Pfam; PF00458; WHEP-TRS; 1.  
 DR PRINTS; PR01039; TRNASYNTHTRP.  
 DR TIGRFAMs; TIGR00233; trps; 1.  
 DR PROSITE; PS00178; AA TRNA LIGASE I; 1.  
 DR PROSITE; PS00762; WHEP-TRS; 1.  
 SQ SEQUENCE 475 AA; 53613 MW; D841D8B26973F214 CRC64;

Query Match 92.3%; Score 1953; DB 2; Length 475;  
 Best Local Similarity 91.2%; Pred. No. 4.1e-148;  
 Matches 365; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 2 NHGPDATAEEDFVDPWMTVOTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRPHHF 61  
 DB 76 NCSDATKASEDFVDPWMTVOTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRPHF 135

QY 62 LRGGIFSHRDMNQVLDAVENKPPFYLTYGRGSPSEAMHGLHPFFFTKWLQDVFNPL 121  
 DB 136 LRGGIFSHRDMNQVLDAVENKPPFYLTYGRGSPSEAMHGLHPFFFTKWLQDVFNPL 195

QY 122 VIQWTDDEKYLWKDLTLDDQAYGDAVENAKDIIACGPDINKTFIFSDLDYMGSSGFYKNV 181  
 DB 196 VIQMSDDEKYLWKDLTLDDQAYSYTVENAKDIIACGPDINKTFIFSDLEYMGQSPGFYRNV 255

QY 182 VKIQKHVTFNQVKGIFGTFDSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCAI 241  
 DB 256 VKIQKHVTFNQVKGIFGTFDSDCIGKISFPAVQAQPSFNSFPKIFRDRDIOCLIPCAI 315

QY 242 DQDPYFMTDRDVPRIQVPRIGYKPKALLHSTFFPALQAGTQMSASDPNSSIFLDTAKQIKTK 301  
 DB 316 DQDPYFMTDRDVPRIQVPRIGYKPKALLHSTFFPALQAGTQMSASDPNSSIFLDTAKQIKSK 375

QY 302 VNKHAFSGGRDTIEHRQFGNCVDVDSFMYLTFFLEDDDKLEQIRKDYTSGLMTGELK 361  
 DB 376 VNKHAFSGGRDTIEHRQFGNCVDVDSFMYLTFFLEDDDLRLQIRKDYTSGLMTGELK 435

RESULT 8  
 Q80ZY4 PRELIMINARY; PRT; 481 AA.

AC Q80ZY4;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)





Query Match 81.9%; Score 1734; DB 2; Length 379;  
Best Local Similarity 92.2%; Pred. No. 1.2e-130;  
Matches 321; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

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QY 1 SNHGPDATAEEDFVDPWTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 60
DB 30 SNGDPDATKASEDFVDPWTVRTSSAKGIDYDKLIVQFGSSKIDKELINRIERATGQRP 89
QY 61 FLRGIFFSHRDMNOVLDAENKPPFLYLTGRGSSSEAMHVGHLIPFIPTKWLQDVNP 120
DB 90 FLRGIFFSHRDMNOVLDAENKPPFLYLTGRGSSSEAMHVGHLIPFIPTKWLQDVNP 149
QY 121 LVIQMTDDEKYLWKDLTDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180
DB 150 LVIQMSDDEKYLWKDLTLEQAYSVTVENAKDIIACGFDVNTKTFISDLEYMGSSGFYKN 209
QY 181 VKIQKHVTNQNKGIFGFTSDCIGKISPAIQAAFSNSFPQIFRDRTDIQCILPCA 240
DB 210 VKIQKHVTNQNKGIFGFTSDCIGKISPAIQAAFSNSFPQIFRDRTDIQCILPCA 269
QY 241 IDQDPYFRMTRDVAPRIGYPKPKALLHSTFFPALQGAQTKMSASDPNSSIFLDTAKQIKT 300
DB 270 IDQDPYFRMTRDVAPRIGHPKPKALLHSTFFPALQGAQTKMSASDPNSSIFLDTAKQIKS 329
QY 301 KVNKHAFSGGRDTIEHRQFGGNCVDVVSFMYLTFLEDDDKLEQIRK 348
DB 330 KVNKHAFSGGRDTVEHRQFGGNCVDVVSFMYLTFLEDDDKLEQIRK 377

RESULT 13
AAH61752
ID AAH61752 PRELIMINARY; PRT; 379 AA.
AC TISSUE=Prostate;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061752; AAH61752.1; -.
KW Hypothetical protein.
SQ SEQUENCE 379 AA; 42880 MW; B9CDB2248780C2E1 CRC64;

Query Match 81.9%; Score 1734; DB 2; Length 379;
Best Local Similarity 92.2%; Pred. No. 1.2e-130;

```

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Matches 321; Conservative 17; Mismatches 10; Indels 0; Gaps 0;
QY 1 SNHGPDATAEEDFVDPWTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 60
DB 30 SNGDPDATKASEDFVDPWTVRTSSAKGIDYDKLIVQFGSSKIDKELINRIERATGQRP 89
QY 61 FLRGIFFSHRDMNOVLDAENKPPFLYLTGRGSSSEAMHVGHLIPFIPTKWLQDVNP 120
DB 90 FLRGIFFSHRDMNOVLDAENKPPFLYLTGRGSSSEAMHVGHLIPFIPTKWLQDVNP 149
QY 121 LVIQMTDDEKYLWKDLTDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180
DB 150 LVIQMSDDEKYLWKDLTLEQAYSVTVENAKDIIACGFDVNTKTFISDLEYMGSSGFYKN 209
QY 181 VKIQKHVTNQNKGIFGFTSDCIGKISPAIQAAFSNSFPQIFRDRTDIQCILPCA 240
DB 210 VKIQKHVTNQNKGIFGFTSDCIGKISPAIQAAFSNSFPQIFRDRTDIQCILPCA 269
QY 241 IDQDPYFRMTRDVAPRIGYPKPKALLHSTFFPALQGAQTKMSASDPNSSIFLDTAKQIKT 300
DB 270 IDQDPYFRMTRDVAPRIGHPKPKALLHSTFFPALQGAQTKMSASDPNSSIFLDTAKQIKS 329
QY 301 KVNKHAFSGGRDTIEHRQFGGNCVDVVSFMYLTFLEDDDKLEQIRK 348
DB 330 KVNKHAFSGGRDTVEHRQFGGNCVDVVSFMYLTFLEDDDKLEQIRK 377

RESULT 14
Q6PBS3
ID Q6PBS3 PRELIMINARY; PRT; 463 AA.
AC Q6PBS3;
RC 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein zgc:73274.
GN Name=zgc:73274;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wild-type; TISSUE=Eye;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wild-type; TISSUE=Eye;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059603; AAH59603.1; -.
DR InterPro; IPR009068; S15/NS1 bind.
DR InterPro; IPR002305; tRNA-synt_1b.

```

DR InterPro; IPR001412; tRNA-synt\_1.  
DR InterPro; IPR002306; ttp tRNA-synt\_1b.  
DR InterPro; IPR000738; WHEP-TRS.  
DR Pfam; PF00579; tRNA-synt\_1b; 1.  
DR Pfam; PF00458; WHEP-TRS; 1.  
DR PRINTS; PR01039; TNASYNTHTRP.  
DR TIGRFAMs; TIGR00233; ttps; 1.  
DR PROSITE; PS00178; AA\_TRNA\_LIGASE\_I; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 463 AA; 52372 MW; ED406A47C9628FEF CRC64;

Query Match 81.9%; Score 1734; DB 2; Length 463;  
Best Local Similarity 81.6%; Pred. No. 1.5e-130;  
Matches 320; Conservative 42; Mismatches 30; Indels 0; Gaps 0;

QY 7 ATAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQPHHFLRGI 66  
DB 70 APQDGEQDVPWSVSSSSAGVDYDKLIVRFGSSKIDKELINRIERATGQPHHFLRGI 129  
QY 67 FFSHRDNQVLDAYENKKPFYLYTGRGPSSEAMHVHGLIPFIPTKWLQDVFNVLVIQMT 126  
DB 130 FFSHRDMHQILDAPFEQKPFYLYTGRGPSQAIHVHGLIPFIPTKWLQDVFNVLVIQMT 189  
QY 127 DDEKYLWKDLTLDOAYGDVAENAKDIACGFDINKTIFSDLDYMGSSGFYKVVVKIQ 186  
DB 190 DDEKYLWKDLTLDECRFTVENARDIACGFDVNVKTFISDLEYMGASPAFYRNWVKVQK 249  
QY 187 HVTFNQVKGIFGFTSDSCIGKISFPALQAAAPSFNSFPQIFRDRDTIOCLIPCAIDODPY 246  
DB 250 HVTFNQVKGIFGFTSDSCIGKISFPALQAAAPSFNSFPQIFGDRKDVQCLIPCAIDODPY 309  
QY 247 FRMTRDVAPRIGYKPKALLHSTFPFALQGAQTKMSASDPNSSIFLTDIAKQIKTKVNKHA 306  
DB 310 FRMTRDVAPRIGYKPKALLHSTFPFALQGAQTKMSASDANSTIFLTDTPQIKNKNVKNHA 369  
QY 307 FSGGRDTIEHRQFGNCVDVVSFMYLTFPLEDDDKLEQIRKDYTSAMLTGELKKALIE 366  
DB 370 FSGGKDTIEHRKLGSDPDVDVSFMYLTFPLEDDDEQLEKIRQDYSSGAMLTGELKSLID 429  
QY 367 VLQPLIAEHQARRKEVTDIVKEFMTPRKLSF 398  
DB 430 TLQPIIAEHQARRKHTDDIVQQFMTPRKLUHF 461

RESULT 15  
AAH59603  
ID AAH59603 PRELIMINARY; PRT; 463 AA.  
AC AAH59603;  
DT 24-MAY-2004 (TrEMBLrel. 27, Created)  
DT 24-MAY-2004 (TrEMBLrel. 27, Last sequence update)  
DT 24-MAY-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein zgc:73274.  
GN ZGC:73274.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=wild-type; TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=wild-type; TISSUE=Eye;  
RA Strausberg R.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC059603; AAH59603.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 463 AA; 52372 MW; ED406A47C9628FEF CRC64;

Query Match 81.9%; Score 1734; DB 2; Length 463;  
Best Local Similarity 81.6%; Pred. No. 1.5e-130;  
Matches 320; Conservative 42; Mismatches 30; Indels 0; Gaps 0;

QY 7 ATAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQPHHFLRGI 66  
DB 70 APQDGEQDVPWSVSSSSAGVDYDKLIVRFGSSKIDKELINRIERATGQPHHFLRGI 129  
QY 67 FFSHRDNQVLDAYENKKPFYLYTGRGPSSEAMHVHGLIPFIPTKWLQDVFNVLVIQMT 126  
DB 130 FFSHRDMHQILDAPFEQKPFYLYTGRGPSQAIHVHGLIPFIPTKWLQDVFNVLVIQMT 189  
QY 127 DDEKYLWKDLTLDOAYGDVAENAKDIACGFDINKTIFSDLDYMGSSGFYKVVVKIQ 186  
DB 190 DDEKYLWKDLTLDECRFTVENARDIACGFDVNVKTFISDLEYMGASPAFYRNWVKVQK 249  
QY 187 HVTFNQVKGIFGFTSDSCIGKISFPALQAAAPSFNSFPQIFRDRDTIOCLIPCAIDODPY 246  
DB 250 HVTFNQVKGIFGFTSDSCIGKISFPALQAAAPSFNSFPQIFGDRKDVQCLIPCAIDODPY 309  
QY 247 FRMTRDVAPRIGYKPKALLHSTFPFALQGAQTKMSASDPNSSIFLTDIAKQIKTKVNKHA 306  
DB 310 FRMTRDVAPRIGYKPKALLHSTFPFALQGAQTKMSASDANSTIFLTDTPQIKNKNVKNHA 369  
QY 307 FSGGRDTIEHRQFGNCVDVVSFMYLTFPLEDDDKLEQIRKDYTSAMLTGELKKALIE 366  
DB 370 FSGGKDTIEHRKLGSDPDVDVSFMYLTFPLEDDDEQLEKIRQDYSSGAMLTGELKSLID 429  
QY 367 VLQPLIAEHQARRKEVTDIVKEFMTPRKLSF 398  
DB 430 TLQPIIAEHQARRKHTDDIVQQFMTPRKLUHF 461

Search completed: January 10, 2005, 21:23:01

Job time : 196 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 10, 2005, 21:16:34 ; Search time 40 Seconds  
(without alignments)  
664.838 Million cell updates/sec

Title: US-09-813-718-10\_COPY\_71\_471

Perfect score: 2116

Sequence: 1 SNHGPPATEAEEDFVDPWT.....VTDEIVKFWTRKUSFDFQ 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCtUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2101	99.3	471	4	US-09-919-039-163
2	1290.5	61.0	401	4	US-09-270-767-45650
3	1218.5	57.6	424	3	US-08-876-885-26
4	774.5	36.6	210	4	US-09-270-767-61162
5	684.5	32.3	255	4	US-09-248-796A-19803
6	550	26.0	213	4	US-09-248-796A-19802
7	195	9.2	338	4	US-09-328-352-4201
8	186	8.8	348	4	US-09-107-532A-5765
9	185.5	8.8	341	3	US-08-928-100-2
10	185.5	8.8	341	3	US-09-492-581-2
11	185.5	8.8	341	4	US-09-425-666-2
12	183.5	8.7	341	4	US-09-563-110-4392
13	174	8.2	335	4	US-09-134-000C-5784
14	164.5	7.8	409	2	US-08-743-130A-39
15	162.5	7.7	409	2	US-08-743-130A-2
16	157.5	7.4	385	4	US-09-489-039A-8660
17	152	7.2	344	4	US-09-198-452A-857
18	141	6.7	346	4	US-09-248-796A-18205
19	132.5	6.3	388	2	US-08-705-868-4
20	132.5	6.3	388	3	US-09-123-615-4
21	123	5.8	356	4	US-09-543-681A-4257
22	118	5.6	349	4	US-09-543-681A-6769
23	118	5.6	426	4	US-09-107-532A-4046
24	113.5	5.4	418	3	US-08-855-910-11
25	113.5	5.4	433	4	US-09-134-000C-3686
26	109	5.2	377	3	US-09-352-990-28
27	108	5.1	197	2	US-08-923-867-2

28	108	5.1	197	3	US-08-928-100-4	Sequence 4, Appli
29	108	5.1	197	3	US-09-183-134-2	Sequence 2, Appli
30	108	5.1	197	3	US-09-492-581-4	Sequence 4, Appli
31	108	5.1	197	4	US-09-425-666-4	Sequence 4, Appli
32	106	5.0	404	4	US-09-248-796A-17676	Sequence 17676, A
33	104.5	4.9	370	2	US-08-415-593-45	Sequence 45, Appl
34	100.5	4.7	421	4	US-09-710-279-1820	Sequence 1820, Ap
35	100.5	4.7	427	3	US-09-134-001C-5141	Sequence 5141, Ap
36	97.5	4.6	335	4	US-09-489-039A-10919	Sequence 10919, A
37	96.5	4.6	374	4	US-09-248-796A-15744	Sequence 15744, A
38	95	4.5	418	3	US-08-844-054-2	Sequence 2, Appli
39	95	4.5	418	3	US-09-347-333-2	Sequence 2, Appli
40	95	4.5	418	4	US-09-583-110-4220	Sequence 4220, Ap
41	95	4.5	459	4	US-09-710-279-1246	Sequence 1246, Ap
42	95	4.5	459	4	US-09-710-279-2554	Sequence 2554, Ap
43	95	4.5	464	3	US-09-134-001C-4701	Sequence 4701, Ap
44	94.5	4.5	877	2	US-08-907-166-8	Sequence 8, Appli
45	94.5	4.5	877	4	US-09-391-340-8	Sequence 8, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-919-039-163  
; Sequence 163, Application US/09919039  
; Patent No. 6727066  
; GENERAL INFORMATION:  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
; FILE REFERENCE: PA-0035 US  
; CURRENT APPLICATION NUMBER: US/09/919,039  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/222,113  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 401  
; SOFTWARE: PERL Program  
; SEQ ID NO 163  
; LENGTH: 471  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6727066 2705515CD1  
US-09-919-039-163

Query Match		99.3%	Score 2101;	DB 4;	Length 471;
Best Local Similarity		99.5%	Pred. No. 3e-227;		
Matches 399;		Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	SNHGPPATEAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP	60		
Db	71	SNHGPPATEAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP	130		
Qy	61	FLRRGIFFSHRDQVLDAYENKKPYLYTGRGSPSEAMHVGHLIPFTKWLQDVNPV	120		
Db	131	FLRRGIFFSHRDQVLDAYENKKPYLYTGRGSPSEAMHVGHLIPFTKWLQDVNPV	190		
Qy	121	LVIQMTDDEKYLKNDLTDOAYGDAVENAKDIIACGPDINKTIFSDLDYMGSSGGYKN	180		
Db	191	LVIQMTDDEKYLKNDLTDOAYGDAVENAKDIIACGPDINKTIFSDLDYMGSSGGYKN	250		
Qy	181	VVKIQKHTVNQVKGIFFGFTDSCIGKISPPAQAPSPNSFPQIFRDRDTDQCLIPCA	240		
Db	251	VVKIQKHTVNQVKGIFFGFTDSCIGKISPPAQAPSPNSFPQIFRDRDTDQCLIPCA	310		
Qy	241	IDQDPYFRMTRDVAIRIGYKPKALLHSTFFPALQGAQTKMSADPNSSIFLTDTAQIKT	300		
Db	311	IDQDPYFRMTRDVAIRIGYKPKALLHSTFFPALQGAQTKMSADPNSSIFLTDTAQIKT	370		
Qy	301	KVNKHAFFSGGRDIEBHRQFGGNCVDVVSFMYLTFLEDDDKLEQTRKDYTSGMLTGEL	360		
Db	371	KVNKHAFFSGGRDIEBHRQFGGNCVDVVSFMYLTFLEDDDKLEQTRKDYTSGMLTGEL	430		

QY 361 KKALIEVLQPLIAHQARRKEVTDIIVKEFTPRKLSFDFQ 401  
 Db 431 KKALIEVLQPLIAHQARRKEVTDIIVKEFTPRKLSFDFQ 471

## RESULT 2

US-09-270-767-45650  
 ; Sequence 45650, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 45650  
 ; LENGTH: 401  
 ; TYPE: PRT  
 ; ORGANISM: *Drosophila melanogaster*  
 ; FEATURE:  
 ; OTHER INFORMATION: Xaa means any amino acid  
 US-09-270-767-45650

Query Match 61.0%; Score 1290.5; DB 4; Length 401;  
 Best Local Similarity 67.4%; Pred. No. 3.6e-136;  
 Matches 240; Conservative 51; Mismatches 64; Indels 1; Gaps 1;  
 QY 7 ATAEEDFVDPWTVQTSAGIDYDKLIVRGSSKIDKELINRIERATGQRPHPFLRGI 66  
 Db 46 ATATEDVDVDPWNVASSNDAGVDYDKLIVRGSSKIDKELIARPEXITGKPAHHFIRRG 105  
 QY 67 FFSHRDNRQVLDAYENKPPFLYTGSGPSSEAMVGHILIPFIETKWLQDVFNVLQMT 126  
 Db 106 FFSHRDLHTLTREOQKPPFLYTGSGPSSEAMVGHILIPFIETKWLQDVFNVLQMT 165  
 QY 127 DDEKYLWKDLTQAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFGYKNVQIK 186  
 Db 166 DDEKTLWKDLKVEDAKILGHENAKDIIAIGFDVKNKTFIENLEFVGKCPAQYQNIIRIQ 225  
 QY 187 HVTFNQVKGIFGFTSDSCIGKISPAIQAAPSFNSFPQIPRDRDTQCLIPCAIDQDPY 246  
 Db 226 CVTFNQVKGIFGFTSDSCIGKISPAIQAAPSFNSFPQIPRDRDTQCLIPCAIDQDPY 284  
 QY 247 FRMTDVAIRIGYPKPAIHLSTFPALQAGTQKMSASDPNSSIFLTDTAKQIKTKVHA 306  
 Db 285 FRMTDVAIRIGYPKPAIHLSTFPALQAGTQKMSASDPNSSIFLTDTAKQIKTKVHA 344  
 QY 307 FSGGRDTIEHRQFGGNCVDVSPWMLTFFLEDDDKLEQIRKDYTGSGAMLTGELKK 362  
 Db 345 FSGGRDTIEHRQFGGNCVDVSPWMLTFFLEDDDKLEQIRKDYTGSGAMLTGELKK 400

## RESULT 3

US-08-876-885-26  
 ; Sequence 26, Application US/08876885  
 ; Patent No. 6174713  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shen, Xiaoyu  
 ; APPLICANT: Homan, Fariba  
 ; TITLE OF INVENTION: CANDIDA CYTOPLASMIC TRYPTOPHANYL-tRNA  
 ; TITLE OF INVENTION: SYNTHETASE PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING  
 ; TITLE OF INVENTION: SAME  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 ; STREET: Two Militia Drive  
 ; CITY: Lexington  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02173

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/876,885  
 FILING DATE: 16-JUN-1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brook, David E.  
 REGISTRATION NUMBER: 22,592  
 REFERENCE/DOCKET NUMBER: CPI97-02  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781) 861-6240  
 TELEFAX: (781) 861-9540  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 424 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-876-885-26

Query Match 57.6%; Score 1218.5; DB 3; Length 424;  
 Best Local Similarity 57.1%; Pred. No. 5e-128;  
 Matches 226; Conservative 71; Mismatches 92; Indels 7; Gaps 3;  
 QY 8 TEAEEDFVDPWTVQ----TSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRPHPFLR 63  
 Db 13 TESEOKITPWEVAGAVDGKSGIDYDKLISQFGTKHITTEILERPKQVTGEPHPFLK 72  
 QY 64 RGIFFFHRDNRQVLDAYENKPPFLYTGSGPSSEAMVGHILIPFIETKWLQDVFNVLQMT 123  
 Db 73 RGVFFSQRLDRLDLVYERGEPEFLYTGSGPSSEAMVGHILIPFIETKWLQDVFNVLQMT 132  
 QY 124 QMTDDKYLWK-DLTLQAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFGYKNV 182  
 Db 133 ELTDDKELFLKHQTLTDDVKGFAENAKDIIAIGFNPENTFIFSDLYMG--GAFYENV 190  
 QY 183 KIQKHTFNQVKGIFGFTSDSCIGKISPAIQAAPSFNSFPQIPRDRDTQCLIPCAID 242  
 Db 191 RTGRQITTTAKAVFGFTSDSCIGKIHFAISQIATAPPSFPDVLGLPPTKCLIPCAID 250  
 QY 243 QDFYFRMTDVAIRIGYPKPAIHLSTFPALQAGTQKMSASDPNSSIFLTDTAKQIKTKV 302  
 Db 251 QDFYFRMTDVAIRIGYPKPAIHLSTFPALQAGTQKMSASDPNSSIFLTDTAKQIKTKV 310  
 QY 303 NKHAFSGGRDTIEHRQFGGNCVDVSPWMLTFFLEDDDKLEQIRKDYTGSGAMLTGELKK 362  
 Db 311 NKYAFSGGRATAEHRQFGGNCVDVSPWMLTFFLEDDDKLEQIRKDYTGSGAMLTGELKK 370  
 QY 363 ALIEVLQPLIAHQARRKEVTDIIVKEFTPRKLSF 398  
 Db 371 ECITVLQEFVSAYQERRSKVDQVVEKFMKPLVLF 406

## RESULT 4

US-09-270-767-61162  
 ; Sequence 61162, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 61162  
 ; LENGTH: 210  
 ; TYPE: PRT  
 ; ORGANISM: *Drosophila melanogaster*



QY 302 VNKHAFSGGRDTHIEHRQFGNCDVDYSEMYLTFLEDDDKLQIRKDYTSGLMGTGELK 361  
Db 224 VNAMYTDPNHLRIEDPGQVEGN-----IVFTYLDADFDPNKEEVELKAHYRRGGLGDTVK 279  
QY 362 KALIEVLOPLIAEHOARKEVTDE 385  
Db 280 KRLEGVLKELITPIRERREBLAKD 303

RESULT 8  
US-09-107-532A-5765  
; Sequence 5765, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 5765:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 348 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (8) LOCATION 1...348  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5765:  
US-09-107-532A-5765

Query Match 8.8%; Score 186; DB 4; Length 348;  
Best Local Similarity 24.9%; Pred. No. 5.5e-12;  
Matches 82; Conservative 57; Mismatches 120; Indels 70; Gaps 14;

QY 88 LYTGRPSSEAMHVGHLIPFTFKWLQDVFNVPVLIQMTDDEKYLWKDLTLDQAVDAVE 147  
Db 17 ILTGDRPTGK-LHLGHYVGS�KTR-----VAMQADENQLFVMIADMQALTDNAK 65  
QY 148 N-----AKDIIACGFDINKT--FIFSDLDYMGMSGFYKNVY---KIQKHVT-- 189  
Db 66 NPEKVSSNVQLVADYLAUGLDPKSTLFIQSIPELAELTWYLYLVSVGRVRRNPTVK 125

QY 190 --FNQVKGIFGFTSDSCIGKISFPAIQAAPSFNSFPQIFRDRTDIQC-LIPCAIDQDPY 246  
Db 126 TEIEQKK---FGESVPTGFFIYVPVQA-----DITAFKANLVPGVGDQKPM 169  
QY 247 FRMTDD-----VAPRIGYKPKALLHSTFFPALOGAQTMSASDPSNSSFILTD 293  
Db 170 LEQTOEIVQSFNHTYGEVLVEPKGVFPKGMGR---LPGIDG-NGKMSKSLGN-GIYISD 224  
QY 294 TAKOIKTKVKNKHAFFSGGRDTIEHRQFGNCDVDYSEMYLTFLEDDDKLEQIRKDYTSG 353  
Db 225 PADVLQKKV-----MSMYTDPNHHVQDPQGVGNMVFYLDVFGTDKEAIEEMKAHYRRG 280  
QY 354 AMLTGELKALIEVLOPLIAEHOARKEV 382  
Db 281 GLGDVKIKRYLIDVLEAFAPIRARREEL 309

RESULT 9  
US-08-928-100-2  
; Sequence 2, Application US/08928100  
; Patent No. 6046174  
; GENERAL INFORMATION:  
; APPLICANT: Gentry, Danile  
; APPLICANT: Greenwood, Claire  
; APPLICANT: Lawlor, Elizabeth  
; TITLE OF INVENTION: No. 6046174el trps  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,100  
; FILING DATE: 12-SEP-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 9619072.3  
; FILING DATE: 12-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gimmi, Edward R  
; REGISTRATION NUMBER: 38,891  
; REFERENCE/DOCKET NUMBER: P31624-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-4478  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 341 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-928-100-2

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Best Local Similarity 24.0%; Pred. No. 6.1e-12;  
Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

QY 84 KPFIYLYTGRPSSEAMHVGHLIPFTFKWLQDVFNVPVLIQMTDDEKY-LWKDLTLDQAY 142  
Db 3 KPIL-TGDRPTGK-LHGHYVGS�KTR-----VLLQEDKYDMFVFLADQAL 49  
QY 143 GDAVEN-----AKDIIACGFDINKTFIF--SDLDYMGMSGFYKNVY---KIQK 186





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; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,130A
; FILING DATE: 01-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CPI95-12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 409 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-743-130A-2

Query Match          7.7%; Score 162.5; DB 2; Length 409;
Best Local Similarity 20.7%; Pred. No. 3.2e-09;
Matches 78; Conservative 59; Mismatches 132; Indels 107; Gaps 16;

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Db   27 IKDVEKENRPVIYNGTAPTKP-HCGYVPWIKLAHFLKAGCEVTLLADLHAFLDNM 85

Qy   118 NVPLVIQMTDEKYLNKDLTLDAQYGDAVENAKDIITACGPDINKTFISDLDTMGWSSGF 177
Db   86 KAPLEVVKYRAKYEFVFKAILKSINVPIERLFVVGVSSYQKGGDYV--MDLFKLSNIV 142

Qy   178 YKNVVK-----IQKHVTFNQVGIGFGTSDCIGKISFPAPAQAPSFSNFPQIFRDRTD 232
Db   143 SQNDKRAGADVVKQVANPLLSELI-----YPLMQA-----IDEEHLG 180

Qy   233 IQCLIPCAIDQDPYFRMTRDVAVRIGPKPALIHSTFFPALOQAQTWMSASDPNSSIFLT 292
Db   181 VDAQFG-GVDQRKI FVLAEENLPSIGYKKRAHLMNPMPVCL-QGGGWMSASDPNSKDII 238

Qy   293 DTAKQIKTKNKHKAFSGG--RDF-----IEEHROPGGN 323
Db   239 EEPPWKVKKNSAYCAPGELKONGLIAFYEVITQPIAELKTGVEGAPKLDIDRPEKYGG- 297

Qy   324 CDVDVSFWMLTFPLEDDDKLEQIRKDYTSGLMTGELKKALI----EVLQPLIAEQARR 379
Db   298 ---PLSY-----DSIEQLKADFVPGKAPPDLKLGVADKINELLAPIRAEPFESS- 343

Qy   380 KEVTDENVKEFMTPRK 395
Db   344 -----EEFQVAK 351

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2005, 21:23:09 ; Search time 145 Seconds  
(without alignments)

997.166 Million cell updates/sec

Title: US-09-813-718-10\_COPY\_71\_471

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Sequence: 1 SNHGPDATAEEDFVDPWT.....VTDEIVKFRTPRKLSDFDQ 401

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
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  - 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2116	100.0	401	14	US-10-080-839-13
2	2116	100.0	415	9	US-09-813-718-14
3	2116	100.0	415	14	US-10-080-839-5
4	2116	100.0	415	15	US-10-240-532-14
5	2116	100.0	415	16	US-10-240-527A-14
6	2116	100.0	437	9	US-09-813-718-12
7	2116	100.0	437	14	US-10-080-839-3
8	2116	100.0	437	15	US-10-240-532-12
9	2116	100.0	437	16	US-10-240-527A-12
10	2116	100.0	471	14	US-10-126-467B-2
11	2116	100.0	471	14	US-10-295-027-1234
12	2116	100.0	471	16	US-10-755-889-250
13	2116	100.0	471	17	US-10-370-715B-250

14	2116	100.0	484	9	US-09-813-718-10	Sequence 10, Appl
15	2116	100.0	484	14	US-10-080-839-1	Sequence 1, Appl
16	2116	100.0	484	15	US-10-240-532-10	Sequence 10, Appl
17	2116	100.0	484	16	US-10-240-527A-10	Sequence 10, Appl
18	2101	99.3	471	10	US-09-919-039-163	Sequence 163, App
19	2101	99.3	471	14	US-10-247-671-166	Sequence 166, App
20	2101	99.3	471	16	US-10-408-765A-1235	Sequence 1235, App
21	2101	99.3	471	17	US-10-733-969A-62	Sequence 62, Appl
22	2101	99.3	475	9	US-09-925-302-558	Sequence 558, App
23	2101	99.3	475	10	US-09-925-302-558	Sequence 558, App
24	1988	94.0	378	14	US-10-080-839-12	Sequence 12, Appl
25	1988	94.0	382	9	US-09-813-718-16	Sequence 16, Appl
26	1988	94.0	382	14	US-10-080-839-7	Sequence 7, Appl
27	1988	94.0	392	15	US-10-240-532-16	Sequence 16, Appl
28	1988	94.0	392	16	US-10-240-527A-16	Sequence 2, Appl
29	1988	94.0	392	17	US-10-628-783-2	Sequence 65, Appl
30	1938	91.6	475	14	US-10-205-219-65	Sequence 120838, Sequence 146807, Sequence 58867, A
31	1326.5	62.7	408	16	US-10-437-963-120838	Sequence 347839, Sequence 8545, App
32	1326	62.7	410	15	US-10-424-593-146807	Sequence 3204, App
33	1302	61.5	429	15	US-10-425-114-58867	Sequence 855, App
34	1200.5	56.7	424	14	US-10-032-585-7632	Sequence 43019, A
35	1168.5	55.2	519	17	US-10-425-115-347839	Sequence 108176, Sequence 298233, Sequence 347838, Sequence 3545, App
36	1125	53.2	433	14	US-10-128-714-8545	Sequence 145795, Sequence 855, App
37	1107.5	52.3	456	15	US-10-320-797-3204	Sequence 855, App
38	831	39.3	173	9	US-09-925-302-855	Sequence 855, App
39	831	39.3	173	10	US-09-925-302-855	Sequence 43019, A
40	710.5	33.6	234	16	US-10-767-701-43019	Sequence 108176, Sequence 298233, Sequence 347838, Sequence 3545, App
41	704.5	33.3	324	16	US-10-437-963-108176	Sequence 108176, Sequence 298233, Sequence 347838, Sequence 3545, App
42	646	30.5	195	17	US-10-425-115-298233	Sequence 108176, Sequence 298233, Sequence 347838, Sequence 3545, App
43	604.5	28.6	192	17	US-10-425-115-347838	Sequence 108176, Sequence 298233, Sequence 347838, Sequence 3545, App
44	414.5	19.6	179	14	US-10-128-714-3545	Sequence 145795, Sequence 855, App
45	398	18.8	137	16	US-10-437-963-145795	Sequence 855, App

ALIGNMENTS

RESULT 1

US-10-080-839-13  
; Sequence 13, Application US/10080839  
; Publication No. US20030017564A1  
; GENERAL INFORMATION:  
; APPLICANT: Schimmel, Paul  
; APPLICANT: Wakaugi, Keisuke  
; APPLICANT: Friedlander, Martin  
; TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived  
; FILE OF INVENTION: Polypeptides Useful For The Regulation of Angiogenesis  
; FILE REFERENCE: TSRI-813.1  
; CURRENT APPLICATION NUMBER: US/10/080, 839  
; PRIOR FILING DATE: 2002-02-22  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-080-839-13

Query Match	100.0%	Score	2116	DB	14	Length	401
Best Local Similarity	100.0%	Pred. No.	3.9e-194				
Matches	401	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	SNHGPDATAEEDFVDPWTVTQTSAGIDYDKLIVRGSSKIDKELINRIERATGQRP	PHH	60			
Db	1	SNHGPDATAEEDFVDPWTVTQTSAGIDYDKLIVRGSSKIDKELINRIERATGQRP	PHH	60			
Qy	61	FLRRGIFFSHRDNNQVLDAYENKKPFYLTGRGSSSAMVGHILPIFTKWLQDVNP	VNP	120			
Db	61	FLRRGIFFSHRDNNQVLDAYENKKPFYLTGRGSSSAMVGHILPIFTKWLQDVNP	VNP	120			
Qy	121	LVQMTEDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFFISDLDYMGSSGFYKN	180				

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Db 121 LVQMDDDEKYLWKDLTLDOAGDAVENAKDIACGFDINKTFIFSDLDYMGSSGFYKN 180
Qy 181 VVKIQHVTNQVKGIFGFTSDSCIGKISFPALQAAPSFNSFPQIFRDRDTIQCLIPCA 240
Db 181 VVKIQHVTNQVKGIFGFTSDSCIGKISFPALQAAPSFNSFPQIFRDRDTIQCLIPCA 240
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLDTAKQIKT 300
Db 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLDTAKQIKT 300
Qy 301 KVNKHAFGSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 360
Db 301 KVNKHAFGSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 360
Qy 361 KKALIEVLOPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 401
Db 361 KKALIEVLOPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 401

RESULT 2
US-09-813-718-14
; Sequence 14, Application US/09813718
; Publication No. US2002018266A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; TITLE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 14
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: supermini Trprs in pET20B
US-09-813-718-14

Query Match 100.0%; Score 2116; DB 9; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPMTVTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 2 SNHGPDTEAEEDFVDPMTVTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 61
Qy 61 FLRRGIFSHRDMNQVLDAYENKPPFLYLTGRGSPSEAMHVGHLPFIPTKWLQDVFNVP 120
Db 62 FLRRGIFSHRDMNQVLDAYENKPPFLYLTGRGSPSEAMHVGHLPFIPTKWLQDVFNVP 121
Qy 121 LVQMDDDEKYLWKDLTLDOAGDAVENAKDIACGFDINKTFIFSDLDYMGSSGFYKN 180
Db 122 LVQMDDDEKYLWKDLTLDOAGDAVENAKDIACGFDINKTFIFSDLDYMGSSGFYKN 181
Qy 181 VVKIQHVTNQVKGIFGFTSDSCIGKISFPALQAAPSFNSFPQIFRDRDTIQCLIPCA 240
Db 182 VVKIQHVTNQVKGIFGFTSDSCIGKISFPALQAAPSFNSFPQIFRDRDTIQCLIPCA 241
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLDTAKQIKT 300
Db 242 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLDTAKQIKT 301
Qy 301 KVNKHAFGSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 360
Db 302 KVNKHAFGSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 361
Qy 361 KKALIEVLOPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 401
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Db 362 KKALIEVLOPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 402

RESULT 3
US-10-080-839-5
; Sequence 5, Application US/10080839
; Publication No. US20030017564A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; APPLICANT: Friedlander, Martin
; TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived
; TITLE OF INVENTION: Polypeptides Useful For The Regulation of Angiogenesis
; FILE REFERENCE: TSRI-813.1
; CURRENT APPLICATION NUMBER: US/10/080,839
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,951
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cleavage Product T1 of recombinant human Trprs
US-10-080-839-5

Query Match 100.0%; Score 2116; DB 14; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPMTVTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 2 SNHGPDTEAEEDFVDPMTVTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 61
Qy 61 FLRRGIFSHRDMNQVLDAYENKPPFLYLTGRGSPSEAMHVGHLPFIPTKWLQDVFNVP 120
Db 62 FLRRGIFSHRDMNQVLDAYENKPPFLYLTGRGSPSEAMHVGHLPFIPTKWLQDVFNVP 121
Qy 121 LVQMDDDEKYLWKDLTLDOAGDAVENAKDIACGFDINKTFIFSDLDYMGSSGFYKN 180
Db 122 LVQMDDDEKYLWKDLTLDOAGDAVENAKDIACGFDINKTFIFSDLDYMGSSGFYKN 181
Qy 181 VVKIQHVTNQVKGIFGFTSDSCIGKISFPALQAAPSFNSFPQIFRDRDTIQCLIPCA 240
Db 182 VVKIQHVTNQVKGIFGFTSDSCIGKISFPALQAAPSFNSFPQIFRDRDTIQCLIPCA 241
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLDTAKQIKT 300
Db 242 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLDTAKQIKT 301
Qy 301 KVNKHAFGSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 360
Db 302 KVNKHAFGSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 361
Qy 361 KKALIEVLOPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 401
Db 362 KKALIEVLOPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 402

RESULT 4
US-10-240-532-14
; Sequence 14, Application US/10240532
; Publication No. US20040009163A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; TITLE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: TSRI 720.1
; CURRENT APPLICATION NUMBER: US/10/240,532
; CURRENT FILING DATE: 2002-09-30
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; PRIOR APPLICATION NUMBER: PCT/US01/08975
; PRIOR APPLICATION NUMBER: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/193,471
; PRIOR APPLICATION NUMBER: 2000-03-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: supermini TrpRS in pET20B
US-10-240-532-14

Query Match      100.0%; Score 2116; DB 15; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 2 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 61
Qy 61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVGHILIPFIYTKWLQDV 120
Db 62 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVGHILIPFIYTKWLQDV 121
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180
Db 122 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 181
Qy 181 VKIQKHVTNQVKGIFGFTSDSCIGKISPPAIOAAPSFNSFPQIFRDRDTIOCLIPCA 240
Db 182 VKIQKHVTNQVKGIFGFTSDSCIGKISPPAIOAAPSFNSFPQIFRDRDTIOCLIPCA 241
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALQGAQTMSASDPNSSIELTDTAKQIKT 300
Db 242 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALQGAQTMSASDPNSSIELTDTAKQIKT 301
Qy 301 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 360
Db 302 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 361
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
Db 362 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 402

RESULT 6
US-09-813-718-12
; Sequence 12, Application US/09813718
; Publication No. US20020182666A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; FILE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human mini
; OTHER INFORMATION: TrpRS in pET20B
US-09-813-718-12

Query Match      100.0%; Score 2116; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.4e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 24 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 83
Qy 61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVGHILIPFIYTKWLQDV 120
Db 84 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVGHILIPFIYTKWLQDV 143
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180
Db 144 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 203
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; PRIOR APPLICATION NUMBER: PCT/US01/08975
; PRIOR APPLICATION NUMBER: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/193,471
; PRIOR APPLICATION NUMBER: 2000-03-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: supermini TrpRS in pET20B
US-10-240-532-14

Query Match      100.0%; Score 2116; DB 15; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 2 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 61
Qy 61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVGHILIPFIYTKWLQDV 120
Db 62 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVGHILIPFIYTKWLQDV 121
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180
Db 122 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 181
Qy 181 VKIQKHVTNQVKGIFGFTSDSCIGKISPPAIOAAPSFNSFPQIFRDRDTIOCLIPCA 240
Db 182 VKIQKHVTNQVKGIFGFTSDSCIGKISPPAIOAAPSFNSFPQIFRDRDTIOCLIPCA 241
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALQGAQTMSASDPNSSIELTDTAKQIKT 300
Db 242 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALQGAQTMSASDPNSSIELTDTAKQIKT 301
Qy 301 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 360
Db 302 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 361
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
Db 362 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 402

RESULT 5
US-10-240-527A-14
; Sequence 14, Application US/10240527A
; Publication No. US20040152079A1
; GENERAL INFORMATION:
; APPLICANT: SCHIMMEL, Paul
; APPLICANT: WAKASUGI, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase
; FILE OF INVENTION: Polypeptides Useful for the Regulation of Angiogenesis
; FILE REFERENCE: TSRI 720.2
; CURRENT APPLICATION NUMBER: US/10/240,527A
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/08966
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/193,471
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human supermini TrpRS in pET20B
US-10-240-527A-14
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181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 240  
Db  
204 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 263  
Qy  
241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKASADPNSSIFLTDTAKQIKT 300  
Db  
264 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKASADPNSSIFLTDTAKQIKT 323  
Qy  
301 KVNKHAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL 360  
Db  
324 KVNKHAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL 383  
Qy  
361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPKLSFDFQ 401  
Db  
384 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPKLSFDFQ 424

## RESULT 7

US-10-080-839-3  
; Sequence 3, Application US/10080839  
; Publication No. US20030017564A1  
; GENERAL INFORMATION:  
; APPLICANT: Schimmel, Paul  
; APPLICANT: Wakasugi, Keisuke  
; APPLICANT: Friedlander, Martin  
; TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived  
; TITLE OF INVENTION: Polypeptides Useful For The Regulation of Angiogenesis  
; FILE REFERENCE: TSRI-813.1  
; CURRENT APPLICATION NUMBER: US/10/080,839  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 60/270,951  
; PRIOR FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; TYPE: PRT  
; LENGTH: 437  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human mini TrpRS in pET20B  
US-10-080-839-3

Query Match 100.0%; Score 2116; DB 14; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.4e-194;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SNHGPDTEAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60  
Db 24 SNHGPDTEAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 83  
Qy 61 FLRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGLIPIFTKWLQDVFNVP 120  
Db 84 FLRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGLIPIFTKWLQDVFNVP 143  
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180  
Db 144 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 203  
Qy 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 240  
Db 204 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 263  
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKASADPNSSIFLTDTAKQIKT 300  
Db 264 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKASADPNSSIFLTDTAKQIKT 323  
Qy 301 KVNKHAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL 360  
Db 324 KVNKHAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL 383  
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPKLSFDFQ 401  
Db 384 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPKLSFDFQ 424

## RESULT 8

US-10-240-532-12  
; Sequence 12, Application US/10240532  
; Publication No. US20040009163A1  
; GENERAL INFORMATION:  
; APPLICANT: Schimmel, Paul  
; APPLICANT: Wakasugi, Keisuke  
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For  
; TITLE OF INVENTION: The Regulation of Angiogenesis  
; FILE REFERENCE: TSRI 720.1  
; CURRENT APPLICATION NUMBER: US/10/240,532  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/08975  
; PRIOR APPLICATION NUMBER: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/193,471  
; PRIOR APPLICATION NUMBER: 2000-03-31  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 437  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: human mini  
; OTHER INFORMATION: TrpRS in pET20B  
US-10-240-532-12

Query Match 100.0%; Score 2116; DB 15; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.4e-194;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SNHGPDTEAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60  
Db 24 SNHGPDTEAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 83  
Qy 61 FLRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGLIPIFTKWLQDVFNVP 120  
Db 84 FLRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGLIPIFTKWLQDVFNVP 143  
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180  
Db 144 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 203  
Qy 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 240  
Db 204 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 263  
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKASADPNSSIFLTDTAKQIKT 300  
Db 264 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKASADPNSSIFLTDTAKQIKT 323  
Qy 301 KVNKHAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL 360  
Db 324 KVNKHAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL 383  
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPKLSFDFQ 401  
Db 384 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPKLSFDFQ 424

## RESULT 9

US-10-240-527A-12  
; Sequence 12, Application US/10240527A  
; Publication No. US20040152079A1  
; GENERAL INFORMATION:  
; APPLICANT: Schimmel, Paul  
; APPLICANT: Wakasugi, Keisuke  
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase  
; TITLE OF INVENTION: Polypeptides Useful for the Regulation of Angiogenesis  
; FILE REFERENCE: TSRI 720.2  
; CURRENT APPLICATION NUMBER: US/10/240,527A

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; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/08966
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/193,471
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human mini TrpRS in pET20B
; US-10-240-527A-12

Query Match      100.0%; Score 2116; DB 16; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.4e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDATAEAEEDFVDPWTQTSSAKGIDYDKLVIRFGSSKIDKELINRIERATGQRP 60
Db 71 SNHGPDATAEAEEDFVDPWTQTSSAKGIDYDKLVIRFGSSKIDKELINRIERATGQRP 130
Qy 61 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSPSSSEAMHVGHLIPFIPTKWLQDV 120
Db 131 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSPSSSEAMHVGHLIPFIPTKWLQDV 190
Qy 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSG 180
Db 191 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSG 250
Qy 181 VVKIQKHVTNQVKGIFGFTSDSCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIPCA 240
Db 251 VVKIQKHVTNQVKGIFGFTSDSCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIPCA 310
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAOTKMSASDPNSSIFLTDTAK 300
Db 311 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAOTKMSASDPNSSIFLTDTAK 370
Qy 301 KVNKHAFIGSGRDTIEHRQFGGNCDDVDSFMYLTFPLEDDDKLBQIRKDYTSGAML 360
Db 371 KVNKHAFIGSGRDTIEHRQFGGNCDDVDSFMYLTFPLEDDDKLBQIRKDYTSGAML 430
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
Db 431 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 471

RESULT 11
US-10-295-027-1234
; Sequence 1234, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 03/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.

; US-10-126-467B-2
; Sequence 2, Application US/10126467B
; Publication No. US2003005979A1
; GENERAL INFORMATION:
; APPLICANT: Paley, Elena
; TITLE OF INVENTION: ANIMAL MODEL OF AND TEST FOR ALZHEIMER'S DISEASE
; FILE REFERENCE: PALL-111
; CURRENT APPLICATION NUMBER: US/10/126,467B
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,980
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/513,895
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 09/384,869
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-126-467B-2

Query Match      100.0%; Score 2116; DB 14; Length 471;
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; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1234
; LENGTH: 471
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-295-027-1234

Query Match      100.0%; Score 2116; DB 14; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.9e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 71 SNHGPDTEAEEDFVDPWTVQTSAGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130
Qy 61 FLRGIFFSHRDNNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTKWLQDV 120
Db 131 FLRGIFFSHRDNNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTKWLQDV 190
Qy 121 LVQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180
Db 191 FLRGIFFSHRDNNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTKWLQDV 190
Qy 301 KVNKHAFFSGGRDITIEHRQFGGNCDDVVSFMYLTFFLEDDDKLEQIRKDYTSGAML 360
Db 371 KVNKHAFFSGGRDITIEHRQFGGNCDDVVSFMYLTFFLEDDDKLEQIRKDYTSGAML 430
Qy 361 KXALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
Db 431 KXALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 471

RESULT 12
US-10-755-889-250
; Sequence 250, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10755,889
; PRIOR FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 250
; LENGTH: 471
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-755-889-250

Query Match      100.0%; Score 2116; DB 16; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.9e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 71 SNHGPDTEAEEDFVDPWTVQTSAGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130
Qy 61 FLRGIFFSHRDNNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTKWLQDV 120
Db 131 FLRGIFFSHRDNNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTKWLQDV 190
Qy 121 LVQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180
Db 191 FLRGIFFSHRDNNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTKWLQDV 190
Qy 301 KVNKHAFFSGGRDITIEHRQFGGNCDDVVSFMYLTFFLEDDDKLEQIRKDYTSGAML 360
Db 371 KVNKHAFFSGGRDITIEHRQFGGNCDDVVSFMYLTFFLEDDDKLEQIRKDYTSGAML 430
Qy 361 KXALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
Db 431 KXALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 471

RESULT 13
US-10-370-715B-250
; Sequence 250, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; APPLICANT: Bodary, Sarah C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 250
; LENGTH: 471
; TYPE: PR
; ORGANISM: Homo sapien
US-10-370-715B-250

Query Match      100.0%; Score 2116; DB 17; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.9e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 71 SNHGPDTEAEEDFVDPWTVQTSAGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130
Qy 61 FLRGIFFSHRDNNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTKWLQDV 120
Db 131 FLRGIFFSHRDNNQVLDAYENKPFYLYTGRGSSSEAMVGHILIPFTKWLQDV 190
Qy 121 LVQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180
Db 191 LVQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 250
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Db 251 VKIQKHVTNQVKGIFGFTDSCIGKISFPALQAAPSFNSFPQIFRDRDIOCLIPCA 310
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSISFLDTAKQIKT 300
Db 311 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSISFLDTAKQIKT 370
Qy 301 KVNKHAFFSGGRDITIEHRQFGGNCDDVVSFMYLTFFLEDDDKLEQIRKDYTSGAML 360
Db 371 KVNKHAFFSGGRDITIEHRQFGGNCDDVVSFMYLTFFLEDDDKLEQIRKDYTSGAML 430
Qy 361 KXALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
Db 431 KXALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 471
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RESULT 15  
US-10-080-839-1  
; Sequence 1, Application US/10080839  
; Publication No. US20030017564A1  
; GENERAL INFORMATION:  
; APPLICANT: Schimmel, Paul  
; APPLICANT: Wakasugi, Keisuke

Search completed: January 10, 2005, 21:35:34  
Job time : 147 secs

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